

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requestor's Name: David Lukton Examiner number: 71263 Date: 5/24/04

Art Unit: 1653 Phone number: 571-272-0952 Serial Number:
09-765105

Mail Box: 3-C-70 Examiner Rm: 3-B-75 Results format: paper

* * * * *

Title of Invention: C-TERMINAL MODIFIED OXAMYL
DIPEPTIDES AS INHIBITORS OF THE ICE-CED-3 FAMILY OF
CYSTEINE PROTEASES

Applicants: KARANEWSKY, DONALD S., TERNANSKY, ROBERT
J., LINTON, STEVEN D., DINH, THANG

Earliest Priority Date: 7/2/98

* * * *

Please search the sequences in this case

182 AA's

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:		NA Sequence (#)	STN
Searcher Phone #:		AA Sequence (#)	Dialog
Searcher Location:		Structure (#)	Questel/Orbit
Date Searcher Picked Up	5/24/04	Bibliographic	Dr. Link
Date Computed:	5/25/04	Litigation	Lexis/Nexis
Searcher Prep & Review Time		Fulltext	Sequence Systems
Clerical Prep Time		Patent Family	QSP
Online Time		Other	WWW/Internet

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions

.rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions

.rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 122770

TO: David Lukton
Location: rem/3b75/3c70
Art Unit: 1653
Tuesday, May 25, 2004

Case Serial Number: 09/765105

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Lukton,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC SEARCH RESULT FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

- I am an examiner in Workgroup: Example: 1610
- Relevant prior art **found**, search results used as follows:
- 102 rejection
 - 103 rejection
 - Cited as being of interest.
 - Helped examiner better understand the invention.
 - Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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OM Protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 51 Seconds
(without alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
Searched: 1585107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB Seq length: 0

Maximum DB Seq length: 2000000000

Post-processing: Maximum Match 0%
Listing First 45 summaries

Database : A_GenSeq_29Jan04.*

1: GeneseqP29Jan04.*
2: GeneseqP1990s.*
3: GeneseqP2000s.*
4: GeneseqP2001s.*
5: GeneseqP2002s.*
6: GeneseqP2003as.*
7: GeneseqP2003bs.*
8: GeneseqP2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	21	AAR34789	4	2	Aar34789 Interleukin
2	21	100.0	4	2	Aar34621 Chromopio
3	21	100.0	4	2	Aar32544 Chromopio
4	21	100.0	4	2	Aar4622 Chromopio
5	21	100.0	4	2	Aar51047 Sequence
6	21	100.0	4	2	Aar77200 Cell pro1
7	21	100.0	4	2	Aar75702 Tetrapept
8	21	100.0	4	2	Aar98753 Asp-ase 1
9	21	100.0	4	2	Aaw00214 Ich-2 sub
10	21	100.0	4	2	Aaw06453 ICE pepti
11	21	100.0	4	2	Aaw5979 Cysteine
12	21	100.0	4	2	Aaw76199 Mouse cas
13	21	100.0	4	2	Aaw52749 Aminomech
14	21	100.0	4	2	Abp1236 ICE-speci
15	21	100.0	4	2	Aaw6304 Peptide C
16	21	100.0	4	2	Aaw5067 ICE bindi
17	21	100.0	4	2	Aay15619 Peptide u
18	21	100.0	4	2	Aay0071 N-substit
19	21	100.0	4	2	Aay04112 Enzyme co
20	21	100.0	4	2	Aaw65555 Interleuk
21	21	100.0	4	2	Aay2410 Caspase P
22	21	100.0	4	2	Aaw99674 ICE prote
23	21	100.0	4	2	Aaw24092 Protease
24	21	100.0	4	2	Aaw94094 Protease
25	21	100.0	4	3	Aay95647 Caspase 1

ALIGNMENTS

RESULT 1	AAR34789 standard; peptide; 4 AA.			
ID	AAR34789			
XX				
AC	AAR34789;			
XX				
DT	25-MAR-2003 (revised)			
DT	08-JUL-1993 (first entry)			
DE	Interleukin-1beta convertase activity determining peptide.			
XX				
KW	ICE; interleukin-1beta convertase; activity; chromophore contg; monitoring; IL-1 mediated diseases; ICE inhibitor evaluation; diagnosis.			
XX				
OS	Synthetic.			
XX				
PH	Key	Location/Qualifiers		
FT	Modified-site	1 /note= "N-acetyl-Tyr"		
FT	Modified-site	4 /note= "Asp-P-nitroanilide, Asp-6-aminoquinoline amide"		
FT	Modified-site	Asp-7-amino-4-methylcoumarin amide"		
XX				
PN	EP33226-A2.			
XX				
PD	24-MAR-1993.			
XX				
PP	08-AUG-1992; 92EP-00202449.			
XX				
PR	16-AUG-1991; 91US-00746524.			
PR	17-DEC-1991; 91US-00808996.			
XX				
PA	(MERCK & CO INC.			
XX				
PI	Chapman KT, MacCoss M, Mumford RA, Thornberry NA, Weidner JR;			
XX				
DR	WPI: 1993-095531/12.			
XX				
CC	New chromophore-contg. Peptide derivs. - for determining interleukin-1-beta convertase activity in the diagnosis of inflammatory and immune-based conditions.			
CC				
CC	Example: Page 26; 41pp; English.			
PS				

The peptide is a chromophore contg. compound which is useful in determining interleukin-1beta convertase (ICE) activity and is therefore useful in diagnosis and monitoring of IL-1 mediated diseases or in evaluation of ICE inhibitors. IL-1 has been implicated in meningitis,

CC salpingitis; complications of septic shock, disseminated intravascular coagulation; adult respiratory distress syndrome, inflammation due to antigen, antibody, and/or complement deposition, arthritis, cholangitis, CC colitis, encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis, pericarditis, pancreatic, reperfusion injury, and vasculitis. Immune based diseases include hypersensitivity, graft rejection, graft-v-host disease, and autoimmune diseases including Type I diabetes mellitus and multiple sclerosis. IL-1 has also been implicated in treatment of bone and cartilage resorption, or diseases causing excessive extracellular matrix deposition. These include periodontal disease, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis, or keloid formation. To use the peptide in an assay, the peptide, ICE, the biological sample, and an aminopeptidase (APAPe) are mixed. The APAPe cleaves the chromophore bond, and the ICE activity is then determined by spectrofluometric or fluorimetric analysis. Leucine amino-peptidase microsomal (LAPM) is the most preferred enzyme in the disclosure. The peptide is used in concns. of 1 μ M to 10 mM. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYAD 4
Db 1 YYAD 4

RESULT 2
AAR34621 ID AAR34621 standard; peptide; 4 AA.
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 12-NOV-1992 (first entry)

DE Chromophore-contg. cpd. for determining ICE activity (1).
XX KW Interleukin-1beta; IL-1b; inflammation; immune; disease; diagnosis;
KW p-nitroanilide.

XX OS Synthetic.

XX PH Key Location/Qualifiers
PT Modified-site 1 /note= "N-acetyl-tyrosyl"

PT Modified-site 4 /note= "aspartic acid 7-amino-4-methylcoumarin"
PN EP528487-A2.

XX PD 24-FEB-1993.
XX DR 08-AUG-1992; 92EP-00202450.
XX PR 16-AUG-1991; 91US-00746455.
XX PR 17-DEC-1991; 91US-00808994.
XX PA (MERI) MERCK & CO INC.

XX PI Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;
PI Hagmann WK;
XX DR 1993-060350/08.

XX PP 08-AUG-1992; 92EP-00202450.
XX PR 16-AUG-1991; 91US-00746455.
XX PR 17-DEC-1991; 91US-00808994.
XX PA (MERI) MERCK & CO INC.

XX PI Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;
PI Hagmann WK;
XX DR 1993-060350/08.

XX PR 16-AUG-1991; 91US-00746455.
XX PR 17-DEC-1991; 91US-00808994.
XX PA (MERI) MERCK & CO INC.

XX PI Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;
PI Hagmann WK;
XX DR 1993-060350/08.

XX PR 16-AUG-1991; 91US-00746455.
XX PR 17-DEC-1991; 91US-00808994.
XX PA (MERI) MERCK & CO INC.

XX PI Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;
PI Hagmann WK;
XX DR 1993-060350/08.

XX PR 16-AUG-1991; 91US-00746455.
XX PR 17-DEC-1991; 91US-00808994.
XX PA (MERI) MERCK & CO INC.

XX Claim 9; Page 42; 42pp; English.

XX The cpd. is used for determining interleukin-1beta convertase (ICE) activity. ICE has been implicated in inflammatory and immune-based diseases including diseases of the lungs and airways, CNS, eyes, ears, joints, bones and connective tissues, cardiovascular system (including the pericardium), GI and urogenital systems and skin and mucosal membranes. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYAD 4
Db 1 YYAD 4

XX

RESULT 3

AAR32544

ID AAR32544 standard; peptide; 4 AA.

XX AC AAR32544;

XX XX

AC AC

XX XX

DT DT 25-MAR-2003 (revised)

XX DT 12-NOV-1992 (first entry)

DE DE Chromophore-contg. cpd. for determining ICE activity (5).

XX XX

KW KW Interleukin-1beta; IL-1b; inflammation; immune; disease; diagnosis;

KW KW 7-amino-4-methylcoumarin.

XX XX

OS OS Synthetic.

XX XX

FH FH Key Location/Qualifiers

PT PT Modified-site 1 /note= "N-acetyl-tyrosyl"

PT PT Modified-site 4 /note= "aspartic acid 7-amino-4-methylcoumarin"

XX XX

PN PN EP528487-A2.

XX XX

PD PD 24-FEB-1993.

XX XX

PR PR 08-AUG-1992; 92EP-00202450.

XX XX

PR PR 16-AUG-1991; 91US-00746455.

XX XX

PR PR 17-DEC-1991; 91US-00808994.

XX XX

PA PA (MERI) MERCK & CO INC.

XX XX

WPI WPI 1993-060350/08.

XX XX

New chromophore-contg. cpds. - for determining interleukin-1beta convertase activity in diagnosis of inflammatory or immune-based disorders.

XX XX

SQ SQ Sequence 4 AA;

Query Match

100.0%; Score 21; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 4
AAR34622 standard; peptide; 4 AA.
ID AAR34622
AC AAR34622;
XX DE Chromophore-contg. cpd. for determining ICE activity (2).
XX Interleukin-1beta; IL-1b; inflammation; immune; disease; diagnosis;
KW 6-aminoquinoline amide.
XX Synthetic.

Key Location/Qualifiers
Modified-site 1 /label= Ac
Modified-site 4 /label= CHO

FT WO9406906-A1.
PD 31-MAR-1994.
PP 09-SEP-1993; 93WO-US008479.
PR 18-SEP-1992; 92US-00947330.
PA (MERCK & CO INC.
PT Molineaux SM, Rolando AM, Casano FU;
PN EP528487-A2.
XX DR WPI: 1994-118456/14.
PD XX DNA encoding murine precursor interleukin 1 beta converting enzyme - for
PT producing ICE and its subunits and for identification of inhibitors of
XX ICE activity.
PS Disclosure; Page 15; 87pp; English.
XX PR 16-AUG-1991; 91US-00746155.
XX PR 17-DEC-1991; 91US-0080394.
XX DR (MERCK & CO INC.
XX PI Chapman KT, Thornberry NA, Maccoso M, Weidner JR, Mumford RA;
PI Hagmann WK;
XX WPI; 1993-060350/08.
XX PT New chromophore-contg. cpds. - for determining interleukin-1beta
PT convertase activity in diagnosis of inflammatory or immune-based
PT disorders.
XX PS Claim 9; Page 42; 42pp; English.
XX CC The cpd. is used for determining interleukin-1beta convertase (ICE)
CC activity. ICE has been implicated in inflammatory and immune-based
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,
CC joints, bones and connective tissues, cardiovascular system (including
CC the pericardium, GI and urogenital systems and skin and mucosal
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 4 AA;

Query Match Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 5
AAR51047 standard; protein; 4 AA.
ID AAR51047

XX AC AAR51047;
XX DT 25-MAR-2003 (revised)
XX DT 07-OCT-1994 (first entry)
XX DE Sequence of tetrapeptide aldehyde inhibitor of murine precursor
DE interleukin-1 beta (pre-IL-1 beta) converting enzyme (ICE).
XX Interleukin-1 beta converting enzyme; mature interleukin; inhibitor; ss.
OS Synthetic.
XX Key Location/Qualifiers
Modified-site 1 /label= Ac
Modified-site 4 /label= CHO

FT XX WO9406906-A1.
PD XX DR WPI: 1994-118456/14.
PP XX PP 09-SEP-1993; 93WO-US008479.
PR XX PR 18-SEP-1992; 92US-00947330.
PA XX PA (MERCK & CO INC.
PT XX PI Molineaux SM, Rolando AM, Casano FU;
PN XX DR WPI: 1994-118456/14.
XX XX DNA encoding murine precursor interleukin 1 beta converting enzyme - for
PT producing ICE and its subunits and for identification of inhibitors of
XX ICE activity.
PS Disclosure; Page 15; 87pp; English.
XX PR 16-AUG-1991; 91US-00746155.
XX DR CC cDNA encoding murine pre-IL-1 beta converting enzyme (ICE) was isolated
CC from IL-1 producing mouse cells. Murine ICE cleaves the peptide bond
CC between Asp117 and Val118 of murine Precursor IL-1 beta, and the peptide
CC bond between Asp27 and Gly28. The preferred cells for isolating murine
CC ICE-encoding DNA include mouse macrophages and (pref.) WEHI-3 cells.
CC Tetrapeptide aldehyde inhibitor Ac-YVAD-CHO inhibits murine ICE with a K_i
CC of 3nM or less. This is comparable to the potency observed against the
CC human enzyme and suggests that the active sites of both convertases are
CC similar. Ac-YVAD-CHO was used to make an affinity ligand (Ac-YVAD-CHO)
CC with which to purify active ICE. Due to the enzyme's unusual substrate
CC specificity, an affinity column can be used to purify ICE in a single
CC step from a crude cellular lysate. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 4 AA;

Query Match Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 6
AAR77200 standard; peptide; 4 AA.
ID AAR77200
XX AC AAR77200;
XX DT 27-FEB-1996 (first entry)
DE Cell proliferation enzyme proteinase activity substrate peptide #5.

RESULT 7
 AAR95702 Standard; peptide: 4 AA.
 AAR95702;
 01-AUG-1996 (first entry)
 Tetrapeptide aldehyde inhibitor 'Ala'.
 Interleukin-1-beta converting enzyme; ICB; inhibitor; inflammation;
 intercellular粘附分子; 炎症; 抑制剂; 血清白细胞介素-1β转化酶

	apoDrosis; protein engineering; City	apoDrosis	apoDrosis	apoDrosis/Qualifiers
XX				
DS				
XX				
Key	Synthetic.			
Key				

PI Horvitz HR, Yuan J, Shaham S;
 XX WPI; 1996-425082/42.
 DR Ced-3 and human interleukin 1-beta convertase genes and proteins - useful
 XX to treat inflammation and diseases characterised by cell death.
 PT Claim 7; Page 94; 139pp; English.

CC A peptide aldehyde including the sequence given in AAR98752, and a
 CC peptide aldehyde designated inhibitor B (AAR98753), are effective,
 CC specific and reversible inhibitors of the protease activity of human
 CC interleukin-1 beta converting enzyme (ICE) (AAR98755) and related
 CC proteases such as nematode Ced-3 (AAR98754). They are thought to act as
 CC transition analogues, which compete for ICE binding to its substrate, pro
 CC -interleukin-1 beta; the Ki for inhibitor B is 0.76 nM. The peptide
 CC aldehydes (Asp-asx inhibitors) inhibit the death of human nerve cells
 CC including motoneurons, and can be used to prevent/decrease cell deaths
 CC due to amyotrophic lateral sclerosis, spinal cord injury, Parkinsonism,
 CC Huntington's disease, Alzheimer's disease or spinocerebellar degeneration
 XX

SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYAD 4
 Db 1 YYAD 4

RESULT 10
 AAW06453 standard; peptide; 4 AA.
 ID AAW06453
 XX AC AAW06453;
 XX DT 03-MAR-1997 (first entry)
 DE ICE Peptide substrate.
 XX KW Ced-3/Ice; cysteine protease; apoptosis; autoimmune disease;
 KW cancer; HIV; Alzheimer's disease; therapy.
 XX OS Synthetic.
 PN WO9636698-A1.
 XX PD 21-NOV-1996.
 XX PP 16-MAY-1996; 96WO-US007010.
 XX PR 18-MAY-1995; 95US-00446925.
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX PI Litwack G, Alnemri ES, Fernandez-Alnemri T;
 XX DR WPI; 1997-012077/01.
 XX PT New isolated apoptotic cysteine protease, Mch 2 - used to develop prods.
 XX PR for uses as anti-apoptotic agents or as cytotoxic agents.
 PS Disclosure; Page 28; 43PP; English.
 XX

RESULT 9
 AAW06453 standard; peptide; 4 AA.
 ID AAW06453
 XX AC AAW06453;
 XX DT 17-NOV-1996 (first entry)
 XX DE Ich-2 substrate.
 XX KW Bih-3; cysteine protease; apoptosis; ICE;
 KW interleukin-1 beta converting enzyme; cancer; tumour; therapy.
 XX OS Synthetic.

PH Key Location/Qualifiers
 FT Modified-site 1 /note= "Tyr at position 1 is pref. acetylated"
 FT Modified-site 4 /note= "Asp at position 4 is pref. modified by a p-
 FT nitroanilide or amino-4-methylcoumarin gp. or Gly-TTP-
 FT amide moiety"
 XX WO9626280-A1.
 XX PD 29-AUG-1996.
 XX PP 21-FEB-1996; 96WO-US002418.
 XX PR 21-FEB-1995; 95US-00391674.
 PR 05-JUN-1995; 95US-00463080.
 XX PA (BADI) BASF AG.
 XX PI Kamens J, Allen H, Paskind M, Mankovich JA, Talanian RV;
 PI Ghayur T;
 XX DR WPI; 1996-402371/40.
 XX PT Isolated Ich-2 cysteine protease, or fragment - may be used to stimulate
 PT apoptosis in cells for research purposes.

XX PS Claim 30; Page 57; 66PP; English.
 XX A synthetic peptide substrate (AAW00214) for a novel human cysteine
 CC protease, termed Ich-2 (see also AAW00213), can be used to identify
 CC modulators of Ich-2 activity. This involves contacting Ich-2 with the
 CC substrate in the presence of a test agent, and measuring Ich-2 protease
 CC activity.
 XX SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YYAD 4
 Db 1 YYAD 4

RESULT 10
 AAW06453 standard; peptide; 4 AA.
 ID AAW06453
 XX AC AAW06453;
 XX DT 03-MAR-1997 (first entry)
 DE ICE Peptide substrate.
 XX KW Ced-3/Ice; cysteine protease; apoptosis; autoimmune disease;
 KW cancer; HIV; Alzheimer's disease; therapy.
 XX OS Synthetic.
 PN WO9636698-A1.
 XX PD 21-NOV-1996.
 XX PP 16-MAY-1996; 96WO-US007010.
 XX PR 18-MAY-1995; 95US-00446925.
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX PI Litwack G, Alnemri ES, Fernandez-Alnemri T;
 XX DR WPI; 1997-012077/01.
 XX PT New isolated apoptotic cysteine protease, Mch 2 - used to develop prods.
 XX PR for uses as anti-apoptotic agents or as cytotoxic agents.
 PS Disclosure; Page 28; 43PP; English.
 XX

A tetrapeptide (AAW06453) is the interleukin-1 beta converting enzyme
 (ICE) cleavage site in pro-interleukin-1 beta. Another tetrapeptide
 (AAW06250) represents a site present in poly(A-ribose) that is cleaved
 by an ICE-like protein during apoptosis. The 2 peptides were used to test
 the activity of human CPP32, ICE and 2 isoforms, alpha (see also
 AAW06245) and beta (AAW06245), of novel human apoptotic cysteine protease
 Mch2. Enzymatic activities were studied in total bacterial extracts from
 cells expressing these enzymes as GST fusion proteins. Neither Mch2 alpha
 nor Mch2 beta was able to cleave the YVAD substrate. Mch2 alpha, but not
 Mch2 beta, cleaved the DEVD substrate, but was 150-fold less active than
 CPP32.
 XX SQ Sequence 4 AA;
 Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YYAD 4

	1	YVAD	4
Db	RESULT 11		
D	AAW45579 standard; peptide; 4 AA.		
AC	AAW45579;		
CX	01-JUL-1998 (first entry)		
CX	Cysteine protease inhibiting peptide for preventing cell death.		
CX	Neuronal cell death; neurodegenerative disorder; inhibition;		
CX	cysteine protease; cardiovascular; liver disease.		
DS	Synthetic.		
CX	WO9735876-A1.		
CX	02-OCT-1997.		
CX	04-MAR-1997; 97WO-US004158.		
CX	04-MAR-1996; 96US-00610220.		
CX	(UYCO) UNIV COLUMBIA NEW YORK.		
PI	Troy CM;		
CX	WPI; 1997-489561/45.		
CX	New cysteine protease inhibiting peptide(s) for preventing cell death - PT in cases of neurodegenerative, cardiovascular and liver diseases, and their peptido-mimetics, and general method for identifying enzyme inhibiting peptides.		
DS	Disclosure; Page 64; 112PP; English.		
CX	This sequence is shown in the specification. The invention relates to peptides of the formula: V-(AA)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5; if n =1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more, (AA1)n-Gln-Ala; X = any amino acid; p = 1-3, depending on value of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n = Arg-Gly-(X)q; q = 1-3, depending on value of m ; V, V', and V'', any or all of which may be absent, = agent able to direct the compound to a specific cell. The peptides are inhibitors of cysteine proteases, specifically interleukin-1 beta converting enzyme (ICE). They inhibit death of cells, particularly in humans, and can be used to treat neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke), cardiovascular disease and liver disorders.		
CX	The peptides should be more specific than pseudosubstrate inhibitors		
3Q	Sequence 4 AA;		
Query Match	100.0%	Score 21; DB 2; Length 4;	
Best Local Similarity	100.0%	Pred. No. 1.4e+06;	
Matches 4;	Conservative 0;	Mismatches 0;	
Indels 0;	Gaps 0;		
DY	1 YVAD	4	
DB	1 YVAD	4	
RESULT 12			
ID	AAW76199 standard; protein; 4 AA.		
CX	AAW76199;		
CX	26-NOV-1998 (first entry)		
Query Match	100.0%	Score 21; DB 2; Length 4;	
Best Local Similarity	100.0%	Pred. No. 1.4e+06;	
Matches 4;	Conservative 0;	Mismatches 0;	
Indels 0;	Gaps 0;		
DY	1 YVAD	4	
DB	1 YVAD	4	
RESULT 13			
ID	AAW52749 standard; peptide; 4 AA..		
XX			
AC	AAW52749;		
XX			
DT	02-MAR-1999 (first entry)		
DE	Aminomethylcoumarin-substituted tetrapeptide.		
XX			
KW	Aminomethylcoumarin; fluorescein; interleukin; ICE; caspase; positional scanning synthetic combinatorial library.		
XX			
OS			
XX			
FH	Key		Location/Qualifiers
FT	Modified-site		/note= "the N-terminal is acetylated"

FT Modified-site 4
 PT /note= "the C-terminal is condensed onto 7-amino- 4-
 methyl-coumarin via an amide linkage"
 XX
 PN GB2324529-A.
 XX
 PD 28-OCT-1998.
 XX
 PF 20-FEB-1998; 98GB-00003559.
 XX
 PR 21-FEB-1997; 97US-0038656P.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Chapman KR, Nicholson D, Rano T, Thornberry N;
 DR WPI; 1998-523841/45.
 XX
 PT New tetrapeptide coumarin derivatives - useful in combinatorial libraries
 PT to identify substrate specificity of cysteine or serine proteases e.g.
 PT interleukin-1 converting enzyme.
 XX
 Claim 3; Page 40; 49pp; English.
 XX
 The peptide is a specifically claimed example of new aminomethyl-
 coumarin-labelled tetrapeptides of formula Ac-Xaa-Xaa-Xaa-Asp-AMC. The
 tetrapeptides are used to generate a fluorescent positional scanning
 synthetic combinatorial library for the investigation of the substrate
 specificity of cysteine and serine proteases e.g. in the analysis of
 interleukin-1 beta converting enzyme substrate and other cyspe
 substrates, and to identify inhibitors which may mediate inflammations.
 CC The library preferably comprises a mixture of at least 200 of the
 CC tetrapeptides
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 14
 ABP71236 standard; peptide; 4 AA.
 XX
 AC ABP71236;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE ICE-specific peptide substrate.
 XX
 KW ICE; sulphonamide; interleukin 1beta converting enzyme; caspase-4;
 KW stroke; inflammatory disease; septic shock; reperfusion injury;
 KW Alzheimer's disease; shigellosis.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 PT /note= "N-terminal acetylation"
 FT Modified-site 4
 PT /note= "C-terminal Asp-PNA"
 XX
 PN WO9816505-A1.
 XX
 PD 23-APR-1998.
 XX
 PR 09-OCT-1997; 97WO-US018396.
 XX

PR 11-OCT-1996; 96US-0028313P.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Albrecht HP, Alien HJ, Brady KD, Harter WG, Kostlan CR, Roth BD,
 PI Walker N;
 XX
 DR WPI; 1998-312002/27.
 XX
 PT New sulphonamide compounds - are inhibitors of interleukin-1beta
 PT converting enzyme and caspase-4, used for treating stroke and
 inflammatory diseases, etc.
 XX
 PS Example 6; Page 35; 59pp; English.
 XX
 The invention provides sulphonamide compounds of specified formula and
 CC their salts, esters, anides and prodrugs. The sulphonamide compounds are
 CC used for inhibiting interleukin 1beta converting enzyme (ICE), inhibiting
 caspase-4, treating or preventing stroke, inflammatory diseases e.g.
 CC arthritis, inflammatory bowel disease, septic shock, reperfusion injury,
 CC Alzheimer's disease and shigellosis. The present sequence represents a
 CC peptide substrate specific for ICE
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 15
 AAW5304
 ID AAW5304 standard; peptide; 4 AA.
 XX
 AC AAW5304;
 XX
 DT 22-JUL-1998 (first entry)
 XX
 DE Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.
 XX
 KW N-acetyl-1-YYAD-methyl coumarinamide; MCA;
 KW interleukin-1- beta converting enzyme-like activity; ICE activity.
 KW cysteine protease; investigation; substrate specificity.
 OS Synthetic.
 XX
 PN JP10099075-A.
 XX
 PD 21-APR-1998.
 XX
 PF 30-SEP-1996;
 XX
 PR 30-SEP-1996;
 XX
 PA (SHIS) SHISEIDO CO LTD.
 XX
 DR WPI; 1998-289868/26.

XX
 Protein with interleukin-1-beta converting enzyme-like activity - useful
 PT in investigation of substrate specificity in, e.g. Parkinson's disease.
 XX
 PS Disclosure; Page 2; 59pp; Japanese.
 XX
 The present sequence, N-acetyl-1-YYAD-methyl coumarinamide (MCA),
 CC represents a sequence that is cleaved by a protein with interleukin-1-
 CC beta converting enzyme (ICE)-like activity. The protein, which is
 CC obtained from human keratinocytes, has a relative molecular weight of 80
 CC kDa. The ICE protein is part of the cysteine protease family and is
 CC useful for investigation of the mechanism of substrate specificity (e.g.

CC Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma,
CC cancer and apoptosis)
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YVAD 4
| |||
Db 1 YVAD 4

Search completed: May 24, 2004, 14:38:15
Job time : 53 secs

Db 1 YVAD 4
RESULT 2

US-08-446-925-10
Sequence 10, Application US/08446925
Patent No. 5672500

GENERAL INFORMATION:
APPLICANT: Litwack, Gerald
APPLICANT: Fernandez-Almendri, Teresa
TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE
ROTENASE, AND COMPOSITIONS FOR MAKING AND
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: USE OF USING THE SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESS: No. 5672500ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446, 925
FILING DATE:

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-4399
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-446-925-10
Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 3
US-08-446-964-1
Sequence 1, Application US/08464964
Patent No. 5716929

GENERAL INFORMATION:
APPLICANT: Lauffer, David J.
APPLICANT: Golec, Julian M.C.
APPLICANT: Mullican, Michael D
APPLICANT: Murcko, Mark A
APPLICANT: Livingston, David J
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA
TITLE OF INVENTION: CONVERTING ENZYME
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464, 964
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261, 452
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI/94-04 CIPPI DIVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE: Modified-site
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "tyrosine is succinylated"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "aspartic acid residue is derivatized with p-nitroanilide"
US-08-464-964-1
Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 4
US-08-446-964-2
Sequence 2, Application US/08464964
Patent No. 5716929
GENERAL INFORMATION:
APPLICANT: Bemis, Guy W.
APPLICANT: Golec, Julian M.C.
APPLICANT: Lauffer, David J.
APPLICANT: Mullican, Michael D
APPLICANT: Murcko, Mark A
APPLICANT: Livingston, David J
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA
TITLE OF INVENTION: CONVERTING ENZYME
NUMBER OF SEQUENCES: 2

APPLICANT: Livingston, David J
 TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr.
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,964
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/440,898
 FILING DATE: 25-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/405,581
 FILING DATE: 17-MAR-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/261,452
 FILING DATE: 17-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9030
 SEQUENCE FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /product= "OTHER"
 /note= "tyrosine is acetylated"

FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /product= "OTHER"
 /note= "aspartic acid is derivatized with
 other information: amino-4-methylcoumarin"
 OTHER INFORMATION:
 US-08-464-964-2

Query Match Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Prd. No. 3e+05; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 1 YVAD 4

RESULT 5
 US-08-700-716-1
 Sequence 1, Application US/08700716
 Patent No. 5744451
 GENERAL INFORMATION:
 APPLICANT: Allen, Hamish J

APPLICANT: Banerjee, Subhashis
 APPLICANT: Brady, Kenneth D
 APPLICANT: Hodges, John C
 APPLICANT: Kostlan, Catherine R
 APPLICANT: Talianan, Robert V
 TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Elizabeth M. Anderson
 STREET: 2800 Plymouth Road
 CITY: Ann Arbor
 STATE: MI
 COUNTRY: US
 ZIP: 48105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Ver 1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/700,716
 FILING DATE: 13-AUG-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Elizabeth M
 REGISTRATION NUMBER: 31585
 REFERENCE/DOCKET NUMBER: PD-5363-01-EMA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313 996-7304
 TELEFAX: 313 996-1553
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-700-716-1

Query Match Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Prd. No. 3e-05; Indels 0; Gaps 0;

Qy 1 YVAD 4
 ||||
 Db 1 YVAD 4

RESULT 6
 US-08-700-716-16
 Sequence 16, Application US/08700716
 Patent No. 5744451
 GENERAL INFORMATION:
 APPLICANT: Banerjee, Subhashis
 APPLICANT: Brady, Kenneth D
 APPLICANT: Hodges, John C
 APPLICANT: Kostlan, Catherine R
 APPLICANT: Talianan, Robert V
 TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Elizabeth M. Anderson
 STREET: 2800 Plymouth Road
 CITY: Ann Arbor
 STATE: MI
 COUNTRY: US
 ZIP: 48105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Ver 1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/700,716
 FILING DATE: 13-AUG-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Elizabeth M.
 REGISTRATION NUMBER: 31:85
 REFERENCE/DOCKET NUMBER: PD-5363-01-EMA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313 996-7304
 TELEX: 313 996-1553
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-700-716-16

RESULT 7
 Best Local Similarity 100.0%; Pred. No. 3e+05; Length 4;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 1 YVAD 4

RESULT 8
 Best Local Similarity 100.0%; Pred. No. 3e+05; Length 4;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 1 YVAD 4

Sequence 4, Application US/08592029
 Patent No. 5763196
 GENERAL INFORMATION:
 APPLICANT: EISENBEIS, SCOTT J.
 ATTORNEY: POWELL, MICHAEL J.
 APPLICANT: KHANNA, PYARE
 APPLICANT: LINGENFELTER, DAVID
 APPLICANT: EISENBEIS, SCOTT J.
 TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE
 TITLE OF INVENTION: FRAGMENTS OF beta-GALACTOSIDASE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/592,029
 FILING DATE: 26-JAN-1996
 CLASSIFICATION: 35
 ATTORNEY/AGENT INFORMATION:
 NAME: MONROY, GLADYS H.
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 33746-20004.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEX: 70611 MRSNFOERS SFO
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

FEATURE: Modified-site
 NAME/KEY: 4
 LOCATION: /product= "OTHER"
 OTHER INFORMATION: /label= Asp-NH-CH₃
 OTHER INFORMATION: /note= "N-methyl aspartic acid"
 FEATURE: Modified-site
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /label= Ac-Tyr
 OTHER INFORMATION: /note= "Acetyl tyrosine"
 US-08-592-029-4

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Length 4;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 1 YVAD 4

RESULT 8
 Sequence 5, Application US/08592029
 Patent No. 5763196
 GENERAL INFORMATION:
 APPLICANT: POWELL, MICHAEL J.
 ATTORNEY: KHANNA, PYARE
 APPLICANT: LINGENFELTER, DAVID
 APPLICANT: EISENBEIS, SCOTT J.
 TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE
 TITLE OF INVENTION: FRAGMENTS OF beta-GALACTOSIDASE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/592,029
 FILING DATE: 26-JAN-1996
 CLASSIFICATION: 35
 ATTORNEY/AGENT INFORMATION:
 NAME: MONROY, GLADYS H.
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 33746-20004.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEX: 70611 MRSNFOERS SFO
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= "Ac-Tyr/
; /note= "Acetyl tyrosine"
US-08-592-029-5

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 9
US-08-777-208-B
Sequence 8, Application US/08777208
Patent No. 5733576

GENERAL INFORMATION:
APPLICANT: Powers, James C.
TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deveau, Colton & Marquis
STREET: Two Midtown Plaza, Suite 1400
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,208
FILING DATE: 27-DEC-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/539444
FILING DATE: 06-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colton, Laurence P.
REGISTRATION NUMBER: 33371
REFERENCE DOCKET NUMBER: 10733-191B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 875-3555
TELEFAX: (404) 875-8505
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
US-08-777-208-B

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 10
US-08-800-007A-11
Sequence 11, Application US/08800007A
Patent No. 5834228
GENERAL INFORMATION:
APPLICANT: Becker, Joseph
APPLICANT: Nicholison, Donald
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR WINDOWS Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,007A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COPPOLA, JOSEPH A.
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 19644
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-800-007A-11

Query Match Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 11
US-08-440-898-1

Sequence 11, Application US/08440898

Patent No. 5847135

GENERAL INFORMATION:
APPLICANT: Benis, Guy W.
APPLICANT: Golec, Julian M.C.
APPLICANT: Laufer, David J.
APPLICANT: Mulligan, Michael D
APPLICANT: Murko, Mark A.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 100-007A-11

CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,898
 FILING DATE: 25-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/405,581
 FILING DATE: 17-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/261,452
 FILING DATE: 25-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-5000
 TELEFAX: 212-596-9050
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /product= "CITER"
 OTHER INFORMATION: /note= "tyrosine is succinylated"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /note= "aspartic acid residue is derivatized with
 p-nitroanilide"
 US-08-440-898-1.

Query Match Score 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 12
 US-08-440-898-2
 ; Sequence 2, Application US/08440898
 ; Patent No. 5647135
 / GENERAL INFORMATION:
 / APPLICANT: Benis, Guy W.
 / APPLICANT: Golec, Julian M.C.
 / APPLICANT: Lauffer, David J.
 / APPLICANT: Mullican, Michael D.
 / APPLICANT: Murcko, Mark A.
 / APPLICANT: Livingston, David J.
 / TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1
 / TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
 / NUMBER OF SEQUENCES: 2
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: James F. Haley Jr.

STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,898
 FILING DATE: 25-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/405,581
 FILING DATE: 17-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/261,452
 FILING DATE: 25-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /note= "tyrosine is acetylated"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /product= "OTHER"
 OTHER INFORMATION: /note= "aspartic acid is derivatized with
 amino-4-methylcoumarin"
 US-08-440-898-2

Query Match Score 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 13
 US-09-057-053-1
 ; Sequence 1, Application US/09067053
 ; Patent No. 5932549
 / GENERAL INFORMATION:
 / APPLICANT: Allen, Hamish J.
 / APPLICANT: Banerjee, Subhasis
 / APPLICANT: Brady, Kenneth D
 / APPLICANT: Hodges, John C
 / APPLICANT: Kostian, Catherine R
 / APPLICANT: Talanian, Robert V
 / TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
 / TITLE OF INVENTION: Beta Converting Enzyme Inhibitory Activity
 / NUMBER OF SEQUENCES: 16
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: James F. Haley Jr.

ADDRESSEE: Elizabeth M. Anderson
 STREET: 2800 Plymouth Road
 CITY: Ann Arbor
 STATE: MI
 ZIP: 48105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Ver 1.36
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/067,053
 FILING DATE: 27-APR-1998
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/700,716
 FILING DATE: 13-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Elizabeth M.
 REGISTRATION NUMBER: 31585
 REFERENCE/DOCKET NUMBER: PD-5363-01-EVA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313 996-1553
 FAX: 313 996-1553
 SEQUENCE FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-067-053-1-L

Query Match Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 14
 US-09-067-053-16
 Sequence 16, Application US/09067053
 GENERAL INFORMATION:
 APPLICANT: Allen, Hamish J.
 APPLICANT: Banerjee, Subhabrata
 APPLICANT: Brady, Kenneth D
 APPLICANT: Hodges, John C
 APPLICANT: Kostlan, Catherine R
 APPLICANT: Talianian, Robert V
 TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Elizabeth M. Anderson
 STREET: 2800 Plymouth Road
 CITY: Ann Arbor
 STATE: MI
 COUNTRY: US
 ZIP: 48105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Ver 1.36
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/067,053
 FILING DATE: 27-APR-1998

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/700,716
 FILING DATE: 13-AUG-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Elizabeth M.
 REGISTRATION NUMBER: 31585
 REFERENCE/DOCKET NUMBER: PD-5363-01-EVA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313 996-1553
 FAX: 313 996-1553
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-067-053-16
 Query Match Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 15
 US-09-146-331-10
 Sequence 10, Application US/09146331
 PATENT NO.: 5958720
 GENERAL INFORMATION:
 APPLICANT: Litwack, Gerald
 APPLICANT: Almendri, Emad S.
 APPLICANT: Hernandez-Almendri, Teresa
 TITLE OF INVENTION: Nch2, AN APOPTOTIC CYSTEINE PROTEASE AND COMPOSITIONS FOR MAKING AND METHODS OF USING THE SAME
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ADDRESS: No. 5958720 R/S
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/146,331
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/896,885
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TUU-1508
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 FAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid

; - TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-146-331-10

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Prcd. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
Db 1 YYAD 4

Search completed: May 24, 2004, 14:38:59
Job time : 16.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode

Run on: May 24, 2004, 14:39:37 : Search time 38 Seconds

(without alignments)
29.360 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters:

1149313

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Published Applications AA:*
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3: /cgnd_6/podata/1/pubpaas/us06_pub.pep:*
4: /cmnd_6/podata/1/pubpaas/us05_pubcomb.pep:*
5: /cmnd_6/podata/1/pubpaas/us07_new_pub.pep:*
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9: /cgnd_6/podata/1/pubpaas/us09a_pubcomb.pep:*
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13: /cgnd_6/podata/1/pubpaas/us09_pubcomb.pep:*
14: /cgnd_6/podata/1/pubpaas/us10_pubcomb.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	4	8	US-09-765-105A-7	Sequence 7, Appli
2	21	100.0	4	9	US-09-799-463-3	Sequence 3, Appli
3	21	100.0	4	9	US-09-735-363A-84	Sequence 8, Appli
4	21	100.0	4	9	US-09-799-994-3	Sequence 3, Appli
5	21	100.0	4	9	US-09-952-768-72	Sequence 72, Appli
6	21	100.0	4	9	US-09-150-623-7	Sequence 7, Appli
7	21	100.0	4	9	US-09-858-754-10	Sequence 10, Appli
8	21	100.0	4	9	US-09-987-417-2	Sequence 2, Appli
9	21	100.0	4	9	US-09-977-831-35	Sequence 35, Appli
10	21	100.0	4	9	US-09-888-443-17	Sequence 17, Appli
11	21	100.0	4	9	US-09-947-872-7	Sequence 2, Appli
12	21	100.0	4	9	US-09-964-114-3	Sequence 3, Appli
13	21	100.0	4	9	US-09-164-114-4	Sequence 4, Appli
14	21	100.0	4	9	US-09-964-114-6	Sequence 6, Appli
15	21	100.0	4	10	US-09-161-172-1	Sequence 1, Appli

SEQUENCE FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

RESULT 1
 US-09-610-220A-7
 Sequence 7, Application US/08610220A
 Publication No. US2003003963BA1
 GENERAL INFORMATION:
 APPLICANT: TROY, Carol M.
 TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
 DEATH AND USES THEREOF
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08610220A
 FILING DATE: MAR-04-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28, 678
 REFERENCE/DOCKET NUMBER: 48332/JPN/JML
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525

MOLECULE TYPE: peptide
 3-08-610-220A-7

Query Match	100
Best Local Similarity	100
Matches	4;
Conservative	

/ 1 YVAD 4
 | |||
 1 YVAD 4

US5-09-735-363A-84

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3-08-610-220A-7

Query Match      100.0%; Score 21; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY:           1 YYAD 4
DB:          1 YYAD 4

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RESULT 2
13-09-799-463-3

PATENT AND TRADEMARK OFFICE / JTA
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Devereaux, Quinn
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.

TITLE OF INVENTION: Apoptosis (IAP) Protein regulation or caspase activity
FILE REFERENCE: LJ 3080
CURRENT APPLICATION NUMBER: US/09/799,463
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 09/058,969
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: 08/862,087
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0

SEQ_ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown
FEATURE:

OTHER INFORMATION : Description of Unknown Organism:Consensus Sequence
5-09-799-463-3 Query Match 100.0% ; Score 21; DB 9; Length 4;

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    1 YVAD 4
    V
    Matches 4; Conservative 0; Mismatches 0;
    Best Local Similarity 100.0%; Pred. No. 1e+05;
    Indels 0; Gaps 0;

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1 YYAD 4

RESULT 3
S-09-735-363A-84
Sequence 84, Application US/09735363A

Patent No. US20010041681A1
GENERAL INFORMATION:
APPLICANT: Filion, Mario
APPLICANT: Phillip, Nicel
TITLE OF INVENTION: Therapeutically Useful
FILE REFERENCE: 0281-0181

CURRENT APPLICATION NUMBER: US/09/735,363A

CORRESPONDENCE ADDRESS: Seed Intellectual Property Law Group
ADDRESSEE: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.3.0

OTHER INFORMATION: Synthetic Peptide

US-09-735-363A-84

Query Match	100.0%	Score 21;	DB 9;	Length 4;
Best Local Similarity	100.0%	Pred. No.	1e+06;	
Matches 4;	Conservative	0;	Mismatches	0;
Qy:	1 YYAD 4			
db:	1 YYAD 4			

RESULT 4
US-09-799-994-3
Sequence 3, Application US/09799994
1 Sequence No. 09799994000000000757A

FACULTY OF NURSING
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Daveroux, Quinn

APPLICANT: Salvessen, Guy S.
APPLICANT: Takahashi, Ryouuke
APPLICANT: ROY, Natalie
TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor Of
TITLE OF INVENTION: Apoptosis (IAP) Protein Regulation Of Caspase Activity
FILED/PRESENTED: 11/2000

Sequence /2, Application US 3,333,278
Patent No. US20020035242A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.

Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomaselli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75

1 CORRESPONDENCE ADDRESS:
1 ADDRESSEE: Seed Inv.
1 STREET: Suite 6300
1 CITY: Seattle
1 STATE: Washington
1 COUNTY: USA
1 ZIP: 98104
1 COMPUTER READABLE FORM:
1 MEDIUM TYPE: Floppies
1 COMPUTER: IBM PC compatibles
1 OPERATING SYSTEM: MS-DOS
1 SOFTWARE: Patent Inv.

APPLICATION NUMBER: US/09/952,768
 FILING DATE: 10-Sep-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Christiansen, William T.
 REGISTRATION NUMBER: 44,614
 REFERENCE/DOCKET NUMBER: 480140.424C4
 TELECOMMUNICATION INFORMATION:
 PHONE: (206) 622-4900
 TELEFAX: (206) 682-0301
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDBEDNESS: <Unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 72:
 US-09-952-768-72

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 6
 US-09-150-023-7
 Sequence 7, Application US/09150623
 Patent No. US2002004491A1
 GENERAL INFORMATION:
 APPLICANT: TROY, CAROL M.
 TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
 NUMBER OF SEQUENCES: 11
 TITLE OF INVENTION: DEATH AND USES THEREOF
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/150,623
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/610,220
 FILING DATE: MAR-04-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 43332/JPW/JML
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDBEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-150-623-7

Query Match 100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 7
 US-09-858-754-10
 Sequence 10, Application US/09858754
 Patent No. US20020055130A1
 GENERAL INFORMATION:
 APPLICANT: Johnson, Gary L.
 TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS
 CURRENT APPLICATION NUMBER: US/09/858,754
 CURRENT FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: 09/023,130
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: 60/039,740
 PRIOR FILING DATE: 1997-02-14
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO: 10
 LENGTH: 4
 TYPE: PRT
 ORGANISM: synthetic construct
 US-09-858-754-10

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 8
 US-09-987-417-2
 Sequence 2, Application US/09987417
 Patent No. US2002005631A1
 GENERAL INFORMATION:
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Weber, Eckard
 APPLICANT: Wang, Yan
 APPLICANT: Mills, Gordon B.
 APPLICANT: Green, Douglas R.
 TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof
 FILE REFERENCE: 1735-0350003
 CURRENT APPLICATION NUMBER: US/09/987,417
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 09/545,565
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: US 60/128,545
 PRIOR FILING DATE: 1999-04-09
 PRIOR APPLICATION NUMBER: US 60/158,370
 PRIOR FILING DATE: 1999-10-12
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: caspase-1 inhibitor
 US-09-987-417-2

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 9
US-09-977-831-35
Sequence 35, Application US/09977831
Patent No. US20021010041
GENERAL INFORMATION:
APPLICANT: PACTT, Tech Transfer Office University of Lausanne
FILE REFERENCE: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
TITLE OF INVENTION: INTRACELLULAR TRANSPORTER PEPTIDES
CURRENT FILING DATE: 2001-10-15
PRIORITY NUMBER: US/09/977.831
PRIORITY NUMBER: U.S.S.N. 60/240,315
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 35
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Caspase
OTHER INFORMATION: Inhibitor Peptide

US-09-977-831-35
Query Match Score 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 10
US-09-888-243-17
Sequence 17, Application US/09888243
Patent No. US2002135714A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Yuan, Junyong
APPLICANT: Shabam, Shai
TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory
TITLE OF INVENTION: Portions of these Genes and Uses Therefor
FILE REFERENCE: 01997/211003
CURRENT APPLICATION NUMBER: US/09/888-243
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 09/083,662
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: US 08/394,189
PRIOR FILING DATE: 1995-02-24
PRIOR APPLICATION NUMBER: US 08/282,211
PRIOR FILING DATE: 1994-07-11
PRIOR APPLICATION NUMBER: US 07/984,182
PRIOR FILING DATE: 1992-11-20
PRIOR APPLICATION NUMBER: US 07/897,788
PRIOR FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 17
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Designed Peptide

US-09-888-243-17
Query Match Score 100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 11
US-09-947-387-2
Sequence 2, Application US/09947387
Patent No. US2002150885A1
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drew, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: Fluorogenic or Fluorescent Reporter Molecule
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735 0290005
CURRENT APPLICATION NUMBER: US/09/947,387
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1998-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 09/168,888
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 2
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
OTHER INFORMATION: Peptide

US-09-947-387-2
Query Match Score 100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 12
US-09-964-114-3
Sequence 3, Application US/09964114
Patent No. US2002156094A1
GENERAL INFORMATION:
APPLICANT: Albrecht, Hans P. et al.
TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme
TITLE OF INVENTION: Inhibitors
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/964,114
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/284,422
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: PCT/US97/18396
PRIOR FILING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: 60/028,313
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 3
LENGTH: 4
TYPE: PRT

ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (1) ..(4)
 OTHER INFORMATION: Acetyl group attached to 5' end and pNA group
 OTHER INFORMATION: attached to 3' end
 OTHER INFORMATION: Description of Artificial Sequence: Chemically
 OTHER INFORMATION: synthesized
 US-09-964-114-3

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 13
 US-09-964-114-4
 Sequence 4, Application US/09964114
 Patent No. US20020156094A1
 GENERAL INFORMATION:
 APPLICANT: Albrecht, Hans P. et al.
 TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/09/964,114
 CURRENT FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: 09/284,422
 PRIOR FILING DATE: 1999-04-02
 PRIOR APPLICATION NUMBER: PCT/US97/18396
 PRIOR FILING DATE: 1999-10-09
 PRIOR APPLICATION NUMBER: 60/028,313
 PRIOR FILING DATE: 1996-10-11
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 4
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (1) ..(4)
 OTHER INFORMATION: Acetyl group attached to 5' end and pNA group
 OTHER INFORMATION: attached to 3' end
 OTHER INFORMATION: Description of Artificial Sequence: Chemically
 OTHER INFORMATION: synthesized
 US-09-964-114-4

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 14
 US-09-964-114-6
 Sequence 6, Application US/09964114
 GENERAL INFORMATION:
 APPLICANT: Albrecht, Hans P. et al.
 TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/09/964,114
 CURRENT FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: 09/284,422
 PRIOR FILING DATE: 1999-04-02

Gencore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on:

May 24, 2004, 14:38:22 ; Search time 175 Seconds
(without alignments)
22.310 Million call updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gap₀ 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

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 33: /cgnd_6_ptodata/2/paa/US60_COMB.pep: *

Sequence 7, Appli

Sequence 10, Appli

Sequence 3, Appli

Sequence 9, Appli

Sequence 3, Appli

Sequence 7, Appli

Sequence 1, Appli

Sequence 26, Appli

Sequence 28, Appli

Sequence 2, Appli

Sequence 36, Appli

Sequence 2, Appli

Sequence 7, Appli

Sequence 1, Appli

Sequence 26, Appli

Sequence 16, Appli

Sequence 17, Appli

Sequence 17, Appli

Sequence 2, Appli

Sequence 3, Appli

Sequence 5, Appli

Sequence 9, Appli

Sequence 13, Appli

Sequence 16, Appli

Sequence 17, Appli

Sequence 17, Appli

Sequence 3, Appli

Sequence 5, Appli

Sequence 10, Appli

Sequence 3, Appli

Sequence 2, Appli

Sequence 10, Appli

Sequence 1, Appli

Sequence 16, Appli

Sequence 17, Appli

Sequence 26, Appli

Sequence 28, Appli

Sequence 26, Appli

ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: caspase-1
PCT-US00-09319-2

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 2 PCT-US01-04137-2

Sequence 2, Application PC/TUS0104137

GENERAL INFORMATION:
APPLICANT: ALEXION PHARMACEUTICALS, INC.

APPLICANT: Fodor, William L.

TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT

FILE REFERENCE: 1097715PCT

CURRENT APPLICATION NUMBER: PCT/US01/04137

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 2

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Caspase

PCT-US01-04137-2

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 3 PCT-US01-04137-3

Sequence 3, Application PC/TUS0104137

GENERAL INFORMATION:
APPLICANT: ALEXION PHARMACEUTICALS, INC.

APPLICANT: Fodor, William L.

TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT

FILE REFERENCE: 1097715PCT

CURRENT APPLICATION NUMBER: PCT/US01/04137

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 3

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Caspase

PCT-US01-04137-3

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4

RESULT 4 PCT-US02-18014-9
Sequence 9, Application PC/TUS0218014
GENERAL INFORMATION:
APPLICANT: Rechsteiner Martin.
APPLICANT: Pratt, Gregory
APPLICANT: Li, Jun
TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS WITH NEURODEGENERATIVE DISEASES RESULTING FROM ABNORMAL PROTEIN
TITLE OF INVENTION: THERAPEUTIC POTENTIAL FOR TREATMENT OF CENTRAL NEURODEGENERATIVE DISEASES
TITLE OF INVENTION: OR PEPTIDE ACCUMULATION
FILE REFERENCE: 21101.0013P1
CURRENT APPLICATION NUMBER: PCT/US02/18014
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/297,332
PRIOR FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 9
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/note =
OTHER INFORMATION: Synthetic construct
PCT-US02-18014-9

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 5 PCT-US02-18484-9
Sequence 9, Application PC/TUS0218484
GENERAL INFORMATION:
APPLICANT: Gibson, Bradford W.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Mitokor
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: ORGANELLAR PROTEOMES INCLUDING DETERMINATION OF TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFICATION IN THE MITOCHONDRIAL PROTEOME USING MASS SPECTROMETRY
TITLE OF INVENTION: IDENTIFICATION OF TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFICATION IN THE MITOCHONDRIAL PROTEOME USING MASS
FILE REFERENCE: 660088 450PCT
CURRENT APPLICATION NUMBER: PCT/US02/18484
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 9
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
NAME/KEY: MOD-RES
LOCATION: (1)-(1)
OTHER INFORMATION: Benzoyl carbonyl moiety
NAME/KEY: MOD-RES
LOCATION: (4)-(4)
OTHER INFORMATION: 7-amino-4-trifluoromethylcoumarin
PCT-US02-18484-9

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 6
 PCT-US02-37577-3
 / Sequence 3, Application PC/TUS0237577
 / GENERAL INFORMATION:
 / APPLICANT: The Burnham Institute
 / APPLICANT: Reed, John C.
 / APPLICANT: Houghten, Richard A.
 / APPLICANT: Nefzi, Adel
 / APPLICANT: Ostresh, John M.
 / APPLICANT: Pinilla, Clemencia
 / APPLICANT: Welsh, Karen
 / TITLE OF INVENTION: Methods and Compositions for
 / TITLE OF INVENTION: Dose-Dependent Activation of IAP-Inhibited Caspase
 / FILE REFERENCE: FP-LJ 5449
 / CURRENT APPLICATION NUMBER: PCT/US02/37577
 / CURRENT FILING DATE: 2002-11-21
 / PRIOR APPLICATION NUMBER: US 60/331,957
 / PRIOR FILING DATE: 2001-11-21
 / NUMBER OF SEQ ID NOS: 5
 / SOFTWARE: FASTSEQ for Windows Version 4.0
 / SEQ ID NO 3
 / LENGTH: 4
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: synthetic construct

PCT-US02-37577-3

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 7
 PCT-US03-20997-7
 / Sequence 7, Application PC/TUS0320997
 / GENERAL INFORMATION:
 / APPLICANT: Wace, EDRIS
 / APPLICANT: Wyeth
 / TITLE OF INVENTION: CASPASE 9 ACTIVATION AND USES THEREFOR
 / FILE REFERENCE: AMI01006 PCT
 / CURRENT APPLICATION NUMBER: PCT/US03/20997
 / CURRENT FILING DATE: 2003-07-08
 / PRIOR APPLICATION NUMBER: 10/191,254
 / PRIOR FILING DATE: 2002-07-08
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 7
 / LENGTH: 4
 / TYPE: PRT
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: Substrate

PCT-US03-20997-7

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 8
 PCT-US96-07010-10
 / Sequence 10, Application PC/TUS9607010
 / GENERAL INFORMATION:
 / APPLICANT: Litwack, Gerald
 / APPLICANT: Alnemri, Emad S.
 / APPLICANT: Fernandez-Alnemri, Teresa
 / TITLE OF INVENTION: Mch2, An APOPTOTIC CYSTEINE PROTEASE, AND COMPOSITIONS FOR MAKING AND METHODS OF USING THE
 / TITLE OF INVENTION: SAME
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Woodcock, Blackburn, Kurtz, Mackiewicz &
 / ADDRESSEE: Norris
 / STREET: One Liberty Place, 46th floor
 / CITY: Philadelphia
 / STATE: PA
 / ZIP: 19103
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WordPerfect 5.1
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: PCT/US96/07010
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/446,925
 / FILING DATE: 18-MAY-1995
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: DeLuca, Mark
 / REGISTRATION NUMBER: 33,229
 / REFERENCE/DOCKET NUMBER: TJU-1882
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (215) 568-3100
 / TELEFAX: (215) 568-3439
 / INFORMATION FOR SEQ ID NO: 10:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 4 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / PCT-US96-07010-10

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 1 YYAD 4

RESULT 9
 PCT-US98-12716-26
 / Sequence 26, Application PC/TUS9812716
 / GENERAL INFORMATION:
 / APPLICANT: Yuan, Junying
 / APPLICANT: Friedlander, Robert M.
 / TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)
 / TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)
 / NUMBER OF SEQUENCES: 28
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Stern, Kessler, Goldstein & Fox P.L.C.

STREET: 1100 New York Avenue NW, Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US98/12716
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/050,242
 FILING DATE: 19-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Jorge A. Goldstein
 REGISTRATION NUMBER: 29,021
 REFERENCE DOCKET NUMBER: 0609.442PC01/JAG/LBB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 LENGTH: 4 amino acids
 SEQUENCE CHARACTERISTICS:
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1 /product= "OTHER"
 OTHER INFORMATION: /label= CHO
 OTHER INFORMATION: /note= "An aldehyde (CHO) group is attached to the C-terminal aspartic acid residue."
 PCT-US98-12716-28
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 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YVAD 4
 Db 1 YVAD 4
 RESULT 11
 PCT-US98-21231-2
 Sequence 2, Application PC/TUS9821231
 GENERAL INFORMATION:
 APPLICANT: Cytovia, Inc.
 TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof
 FILE REFERENCE: 1735.029PC02
 CURRENT APPLICATION NUMBER: PCT/US98/21231
 CURRENT FILING DATE: 1998-10-09
 EARLIER APPLICATION NUMBER: US 09/033,661
 EARLIER FILING DATE: 1997-10-10
 NUMBER OF SEQ ID NOS: 142
 SEQ ID NO: 2
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide
PCT-US98-21231-2

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.Se+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
Db 1 YYAD 4

RESULT 12
PCT-US99-08064-36

Sequence 36, Application PC/TUS9908064A

GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Morishima, Nobuhiro
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: Programmed Cell Death and Caspase-12
FILE REFERENCE: 0609-440PC01
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: US 6,0/081,962
EARLIER FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
PCT-US99-08064-36

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.Se+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
Db 1 YYAD 4

RESULT 13
PCT-US99-16423-2

Sequence 2, Application PC/TUS9916423

GENERAL INFORMATION:
APPLICANT: Cytovia, Inc.
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui-Xiong
APPLICANT: DREW, John A.
APPLICANT: YANG, Wu

TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
FILE REFERENCE: 1735.103PC01
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: PCT/US99/16423
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetet-C
OTHER INFORMATION: Peptide
PCT-US99-16423-2

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
Db 1 YYAD 4

RESULT 14
US-08-183-269-1
Sequence 1, Application US/08183269

GENERAL INFORMATION:
APPLICANT: Molinaux, Susan M.
APPLICANT: Rolando, Anna M.
APPLICANT: Casano, Francesca J.
TITLE OF INVENTION: DNA Encoding Murine Precursor
TITLE OF INVENTION: Interleukin 1 Beta Converting Enzyme
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//08/183,269
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,330
FILING DATE: 18-SEP-1992
ATTORNEY AGENT INFORMATION:
NAME: Wallen, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 18857
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-183-269-1

Query Match Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
Db 1 YYAD 4

RESULT 15
US-08-282-211A-16
Sequence 16, Application US/08282211A

GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Yuan, Junying
APPLICANT: Shaham, Shai
TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1
TITLE OF INVENTION: CONVERTASE GENE TO A C. ELEGANS CELL DEATH GENE
TITLE OF INVENTION: INHIBITORY PORTIONS OF THESE GENES AND USES THEREFOR

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2604
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,211A
FILING DATE: 11-JUL-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE DOCKET NUMBER: 01997/198004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-282-211A-16

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Fred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YVAD 4
Db 1 YVAD 4

Search completed: May 24, 2004, 14:47:41
Job time : 176 secs

GenCore version 5.1.6
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OM Protein - protein search, using sw model
 Run on: May 24, 2004, 14:39:07 ; Search time 13.5 Seconds
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 10.992 Million cell updates/sec

Title: US-09-765-105A-1
 Perfect score: 21
 Sequence: 1 YVAD 4

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 251736

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 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

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 9: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 10: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 11: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 12: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 13: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 14: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 15: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 16: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 17: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
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 19: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 20: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 21: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 22: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 23: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 24: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 25: /cgn2_6/ptodata/1/paa/us628_new comb.pep:
 26: /cgn2_6/ptodata/1/paa/us628_new comb.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	4	1	PCT-US03-41600-528	Sequence 528, APP
2	21	100.0	4	6	US-10-627-556-328	Sequence 528, APP
3	21	100.0	4	6	US-10-630-326-15	Sequence 15, APP
4	21	100.0	4	6	US-10-829-381-2	Sequence 2, APP
5	21	100.0	4	6	US-10-665-668A-7	Sequence 7, APP
6	21	100.0	5	6	US-10-829-381-7	Sequence 72, APP
7	21	100.0	5	6	US-10-665-668A-6	Sequence 6, APP
8	21	100.0	6	6	US-10-829-381-142	Sequence 142, APP
9	21	100.0	14	5	US-09-394-019B-42	Sequence 42, APP
10	21	100.0	14	5	US-09-394-019B-43	Sequence 43, APP
11	21	100.0	14	5	US-09-394-019B-287	Sequence 287, APP
12	21	100.0	14	5	US-09-394-019B-288	Sequence 288, APP
13	21	100.0	14	5	US-09-394-019B-42	Sequence 4, APP
14	21	100.0	14	5	US-09-394-019B-43	Sequence 43, APP
15	21	100.0	14	5	US-09-394-019C-42	Sequence 42, APP
16	21	100.0	14	5	US-09-394-019C-43	Sequence 4, APP
17	21	100.0	14	5	US-09-394-019C-287	Sequence 287, APP
18	21	100.0	14	5	US-09-394-019C-288	Sequence 288, APP
19	21	100.0	16	5	US-09-394-019B-45	Sequence 45, APP
20	21	100.0	16	5	US-09-394-019B-46	Sequence 46, APP
21	21	100.0	16	5	US-09-394-019B-290	Sequence 290, APP
22	21	100.0	16	5	US-09-394-019B-291	Sequence 291, APP
23	21	100.0	16	5	US-09-394-019B-45	Sequence 46, APP
24	21	100.0	16	5	US-09-394-019C-45	Sequence 45, APP
25	21	100.0	16	5	US-09-394-019C-46	Sequence 46, APP
26	21	100.0	16	5	US-09-394-019C-46	Sequence 46, APP

RESULT 1
 PCT-US03-41600-528, Application PC/TUS0341600
 ; Sequence 528, Application PC/TUS0341600
 ; GENERAL INFORMATION:
 ; APPLICANT: TRUBION PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
 ; FILE REFERENCE: 49076.000004.CIP/PCT
 ; CURRENT APPLICATION NUMBER: PCT-US03/41600
 ; CURRENT FILING DATE: 2003-12-24
 ; PRIOR APPLICATION NUMBER: 10/1627, 556
 ; PRIOR FILING DATE: 2003-07-26
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 528
 ; LENGTH: 4
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; PCT-US03-41600-528

RESULT 2
 US-10-627-556-528, Application US/10627556
 ; Sequence 528, Application US/10627556
 ; GENERAL INFORMATION:
 ; APPLICANT: LEDBETTER, JEFFREY A., MARTHA
 ; APPLICANT: THOMPSON, PETER A., HAYDEN-JEDBECKER,
 ; APPLICANT: THOMPSON, PETER A., HAYDEN-JEDBECKER, MARTHA
 ; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
 ; FILE REFERENCE: 49076.000004.CIP2
 ; CURRENT APPLICATION NUMBER: US/10/627, 556
 ; CURRENT FILING DATE: 2003-07-26
 ; PRIOR APPLICATION NUMBER: 10/053, 530
 ; PRIOR FILING DATE: 2002-01-17
 ; PCTOR APPLICATION NUMBER: 60/367, 358
 ; PRIOR FILING DATE: 2002-01-16
 ; PRIOR APPLICATION NUMBER: 09/765, 208
 ; PRIOR FILING DATE: 2001-01-17
 ; PCTOR APPLICATION NUMBER: 60/385, 691
 ; PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2000-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 528
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-627-556-528

Query Match Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 3
US-10-630-926-15
; SEQUENCE: Application US/10630926
; GENERAL INFORMATION:
; APPLICANT: RICCIARDI, Carlo
; TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL DEATH PATHWAYS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.1, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/630,926
; FILING DATE: 31-JUL-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/403,861A
; FILING DATE: 11-FEB-2000
; APPLICATION NUMBER: PCT/EP98/02490
; FILING DATE: 27-APR-1998
; APPLICATION NUMBER: EP 97107033, 9
; FILING DATE: 28-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: YIN, Allen C.
; REGISTRATION NUMBER: 37,971
; RECOMMENDATION NUMBER: RICCARDI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-377-5298
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with CH2OC(O)-[2,6-(CF3)2]Ph"

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-630-926-15

Query Match Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 4
US-10-829-381-2
; Sequence 2, Application US/10829381
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John P.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; FILE REFERENCE: 1735_0290006
; CURRENT APPLICATION NUMBER: US/10/829,381
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 09/947,387
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 142
; SEQ ID NO: 2
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-829-381-2

Query Match Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 1 YVAD 4

RESULT 5
US-10-665-668A-7
; Sequence 7, Application US/10665668A
; GENERAL INFORMATION:
; APPLICANT: TROY, CAROL M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF
; FILE REFERENCE: 057548332-B
; CURRENT APPLICATION NUMBER: US/10/665,668A
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MOTIF OF PSEUDOSUBSTRATE INHIBITOR
US-10-665-668A-7

Query Match Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-10-829-381-72
Sequence 72, Application US/10629381
 / GENERAL INFORMATION:
 / APPLICANT: Weber, Eckard
 / APPLICANT: Cai, Sui Xiong
 / APPLICANT: Keana, John F.W.
 / APPLICANT: Drewe, John A.
 / APPLICANT: Zhang, Han-Zhong
 / TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof
 / TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the Use Thereof
 / FILE REFERENCE: 1735.090006
 / CURRENT APPLICATION NUMBER: US/10/829,381
 / CURRENT FILING DATE: 2004-04-22
 / PRIOR APPLICATION NUMBER: US 60/061,582
 / PRIOR FILING DATE: 1997-10-10
 / PRIOR APPLICATION NUMBER: US 60/145,746
 / PRIOR FILING DATE: 1998-03-03
 / PRIOR APPLICATION NUMBER: US 09/168,888
 / PRIOR FILING DATE: 1998-10-09
 / PRIOR APPLICATION NUMBER: US 09/169,888
 / PRIOR FILING DATE: 1998-10-09
 / PRIOR APPLICATION NUMBER: US 09/947,387
 / PRIOR FILING DATE: 2001-09-07
 / NUMBER OF SEQ ID NOS: 142
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 72
 / LENGTH: 5
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 / OTHER INFORMATION: Peptide
 US-10-829-381-72
 Query Match 100.0%; Score 21; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 1 YYAD 4
 Db 1 YYAD 4

RESULT 8
US-10-829-381-142
Sequence 142, Application US/10629381
 / GENERAL INFORMATION:
 / APPLICANT: Weber, Eckard
 / APPLICANT: Cai, Sui Xiong
 / APPLICANT: Keana, John F.W.
 / APPLICANT: Drewe, John A.
 / APPLICANT: Zhang, Han-Zhong
 / TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof
 / TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the Use Thereof
 / FILE REFERENCE: 1735.090006
 / CURRENT APPLICATION NUMBER: US/10/829,381
 / CURRENT FILING DATE: 2004-04-22
 / PRIOR APPLICATION NUMBER: US 60/061,582
 / PRIOR FILING DATE: 1997-10-10
 / PRIOR APPLICATION NUMBER: US 60/145,746
 / PRIOR FILING DATE: 1998-03-03
 / PRIOR APPLICATION NUMBER: US 09/168,888
 / PRIOR FILING DATE: 1998-10-09
 / PRIOR APPLICATION NUMBER: US 09/947,387
 / PRIOR FILING DATE: 2001-09-07
 / NUMBER OF SEQ ID NOS: 142
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 142
 / LENGTH: 6
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence:Synthetic
 / OTHER INFORMATION: Peptide
 US-10-829-381-142
 Query Match 100.0%; Score 21; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 1 YYAD 4
 Db 1 YYAD 4

RESULT 9
US-09-394-019B-42
Sequence 42, Application US/09394019B
 / GENERAL INFORMATION:
 / APPLICANT: Oncoimmunin, Inc.
 / APPLICANT: Konorova, Akira
 / APPLICANT: Packard, Beverly
 / TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES AND METHODS OF USE THEREOF
 / FILE REFERENCE: 300-90320US
 / CURRENT APPLICATION NUMBER: US/09/394,019B
 / CURRENT FILING DATE: 1999-05-10
 / PRIOR APPLICATION NUMBER: PCT/US98/00300
 / PRIOR FILING DATE: 1998-02-20
 / PRIOR APPLICATION NUMBER: US 08/602,981
 / NUMBER OF SEQ ID NOS: 405
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO: 42
 / LENGTH: 14
 / TYPE: PRT
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: Synthetic peptide substrate

RESULT 7
US-10-665-668A-6
Sequence 6, Application US/10665668A
 / GENERAL INFORMATION:
 / APPLICANT: TROY, CAROL M.
 / TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF
 / FILE REFERENCE: 0575/48332-B
 / CURRENT APPLICATION NUMBER: US/10/665,668A
 / CURRENT FILING DATE: 2003-09-19
 / NUMBER OF SEQ ID NOS: 11
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO: 6
 / LENGTH: 5
 / TYPE: PRT
 / ORGANISM: artificial sequence
 / FEATURE:
 / OTHER INFORMATION: COMPETITIVE INHIBITOR OF ICE

US-10-665-668A-6
 Query Match 100.0%; Score 21; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 1 YYAD 4

NAME/KEY: MOD_RBS
 LOCATION: (3) .(3)
 OTHER INFORMATION: X is Aib
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (3) .(3)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 US-09-394-019B-42

Query Match Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 4 YVAD 7

RESULT 10
 Sequence 43, Application US/09394019B
 GENERAL INFORMATION:
 APPLICANT: Oncoimmunin, Inc.
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly
 TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
 FILE REFERENCE: 300-903820US
 CURRENT FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: US/09/394,019B
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: PCT/US98/00300
 PRIOR FILING DATE: 1998-02-20
 NUMBER OF SEQ ID NOS: 405
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 43
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic peptide substrate
 FEATURE:
 NAME/KEY: MOD_RFS
 LOCATION: (3) .(3)
 OTHER INFORMATION: X is Aib
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (3) .(3)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 US-09-394-019B-43

Query Match Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 4 YVAD 7

RESULT 11
 Sequence 287, Application US/09394019B
 GENERAL INFORMATION:
 APPLICANT: Oncoimmunin, Inc.
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly
 TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
 FILE REFERENCE: 300-903820US
 CURRENT FILING DATE: 1999-09-10
 NUMBER OF SEQ ID NOS: 405
 SOFTWARE: PatentIn version 3.2

PRIOR APPLICATION NUMBER: PCT/US98/00300
 PRIOR FILING DATE: 1998-02-20
 NUMBER OF SEQ ID NOS: 405
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 287
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic peptide. Chemically synthesized protease substrate.

Query Match Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 4 YVAD 7

RESULT 12
 Sequence 288, Application US/09394019B
 GENERAL INFORMATION:
 APPLICANT: Oncoimmunin, Inc.
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly
 TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
 FILE REFERENCE: 300-903820US
 CURRENT APPLICATION NUMBER: US/09/394,019B
 CURRENT FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: PCT/US98/00300
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: US 08/802,981
 PRIOR FILING DATE: 1997-02-20
 NUMBER OF SEQ ID NOS: 405
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 288
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic peptide. Chemically synthesized protease substrate.

Query Match Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 4 YVAD 7

RESULT 13
 Sequence 42, Application US/09394019B
 GENERAL INFORMATION:
 APPLICANT: Oncoimmunin, Inc.
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly
 TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
 FILE REFERENCE: 300-903820US
 CURRENT APPLICATION NUMBER: US/09/394,019B
 CURRENT FILING DATE: 1999-09-10

TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
 FILE REFERENCE: M-903820US
 CURRENT FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: PCT/US98/00300
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: US 08/802,981
 NUMBER OF SEQ ID NOS: 257
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 42
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic peptide substrate
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (3) .(3)
 OTHER INFORMATION: Xaa is Aib
 US-09-394-019B-42

Query Match 100.0%; Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YVAD 4
 Db 4 YVAD 7

RESULT 14
 US-09-394-019B-43
 Sequence 43, Application US/09394019B
 GENERAL INFORMATION:
 APPLICANT: Oncoimmunin, Inc.
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly
 TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
 FILE REFERENCE: M-903820US
 CURRENT FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: PCT/US98/00300
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: US 08/802,981
 NUMBER OF SEQ ID NOS: 257
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 43
 LENGTH: 14
 TYPE: PRT

FEATURE:
 OTHER INFORMATION: Synthetic peptide substrate
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (3) .(3)
 OTHER INFORMATION: Xaa is Aib
 US-09-394-019B-43

Query Match 100.0%; Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YVAD 4
 Db 4 YVAD 7

RESULT 15
 US-09-394-019C-42

Sequence 42, Application US/09394019C
 GENERAL INFORMATION:
 APPLICANT: Oncoimmunin, Inc.
 APPLICANT: Komoriya, Akira
 APPLICANT: Packard, Beverly
 TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
 FILE REFERENCE: M-903820US
 CURRENT FILING DATE: 1999-09-10
 CURRENT APPLICATION NUMBER: US/09/394,019C
 PRIOR APPLICATION NUMBER: PCT/US98/00300
 PRIOR FILING DATE: 1998-02-20
 PRIOR APPLICATION NUMBER: US 08/802,981
 NUMBER OF SEQ ID NOS: 405
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 42
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic peptide substrate
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (3) .(3)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (3) .(3)
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 US-09-394-019C-42

Query Match 100.0%; Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YVAD 4
 Db 4 YVAD 7

Query Match 100.0%; Score 21; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YVAD 4
 Db 4 YVAD 7

Search completed: May 24, 2004, 14:48:20
 Job time : 13.5 secs

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OM Protein - protein search, using sw mode!
Run on: May 24, 2004, 14:36:18 ; Search time 13.5 Seconds
(without alignments)
28.501 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	32	S20719	alcohol dehydrogenase related protein (EC 1.1.1.-) - fruit fly (Drosophila yakuba) (fr)
2	21	100.0	43	A24553	N; Alternate names: Adh-dup protein; Adh-related protein; Adhr protein; alcohol dehydrogenase
3	21	100.0	54	H82718	C; Species: Drosophila yakuba
4	21	100.0	66	PC4222	C; Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 11-Jun-1999
5	21	100.0	66	PC4266	R; Accession: S20719
6	21	100.0	68	G82969	R; Ashburner, M.
7	21	100.0	75	AC1251	Submitted to the EMBL Data Library, July 1990
8	21	100.0	76	S51629	A; Reference number: S20713
9	21	100.0	77	R3BS18	A; Accession: S20719
10	21	100.0	80	AC1613	A; Molecule type: DNA
11	21	100.0	82	I51103	A; Residues: 1-32 <ASH>
12	21	100.0	82	I51106	A; Cross-references: EMBL:X54120; PIDN:CAA38064.1; PMID:99216
13	21	100.0	82	E71321	C; Genetics:
14	21	100.0	86	A28093	A; Gene: FlyBase:Adhr; Adh-dup
15	21	100.0	88	S71291	A; Cross-references: FlyBase:FBgn0013164
16	21	100.0	88	H77560	C; SuperFamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
17	21	100.0	94	G69957	C; Keywords: oxidoreductase
18	21	100.0	94	AE2197	
19	21	100.0	95	A49027	
20	21	100.0	97	H42409	
21	21	100.0	97	AD2153	
22	21	100.0	98	F97952	
23	21	100.0	99	AG8437	
24	21	100.0	101	A47450	
25	21	100.0	102	T29100	
26	21	100.0	102	B89860	
27	21	100.0	106	D50247	
28	21	100.0	112	C33766	
29	21	100.0	113	D27664	

ALIGNMENTS

RESULT 1							
S20719	alcohol dehydrogenase related protein (EC 1.1.1.-) - fruit fly (Drosophila yakuba) (fr)	N; Alternate names: Adh-dup protein; Adh-related protein; Adhr protein; alcohol dehydrogenase	C; Species: Drosophila yakuba	C; Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 11-Jun-1999	R; Ashburner, M.	Submitted to the EMBL Data Library, July 1990	
						A; Reference number: S20713	A; Accession: S20719
						A; Molecule type: DNA	A; Residues: 1-32 <ASH>
						A; Cross-references: EMBL:X54120; PIDN:CAA38064.1; PMID:99216	C; Genetics:
						A; Gene: FlyBase:Adhr; Adh-dup	A; Cross-references: FlyBase:FBgn0013164
						C; SuperFamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology	C; Keywords: oxidoreductase
Query	Match	Score	21;	DB 2;	Length	32;	
Qy	Best Local Similarity	100.0%	Pred. No.	54;	Mismatches	0;	Indels 0; Gaps 0;
	Matches	4;	Conservative	0;			
Db	11	YVAD 14					

RESULT 2							
A24553	cuticule protein SC1 - flesh fly (Sarcophaga bullata) (fragment)	C; Species: Sarcophaga bullata	C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 18-Jun-1993	R; Henzel, W.J.; Moile, J.E.; Mulligan, K.; Lipe, H.	J. Mol. Evol. 22, 39-45, 1985	A; Title: Sarcophagid larval Proteins: Partial sequence homologies among three cuticle proteins	A; Reference number: A92963; MUID:86037264; PMID:3932263
Qy	1 YVAD 4						
Db	11 YVAD 14						

Query Match							
Qy	Best Local Similarity	100.0%	Pred. No.	74;	Mismatches	0;	Indels 0; Gaps 0;
	Matches	4;	Conservative	0;			
Db	1 YVAD 4						

RESULT 3

RESULT 5

HB2718 hypothetical protein XP_1129 [Imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: HB2718

R;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A8515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: HB2718

A;Status: preliminary

A;Residues: 1-54 <NIS>

A;Cross-references: GB:AEE003849; GB:AE003849; NID:9106088; PIDN:AAF83939.1; GSPDB:GN001

R;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.; Bueno, M.R.P.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H.

as Pedro, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, S.C.; Franca, M.C.; Frohn,

J.D.; Junqueira, M.L.; Kempter, B.L.; Kitajima, J.B.; Kuramae, E.E.; Laige-

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.F.; Marinho, C.L.; Marques, M.V.; Martins,

E.; Martínez, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

I.F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, R.C.; Palimieri, D.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; Santelli, R.V.; Sawasaki

M.; Tsubakio, M.H.; Vallada, H.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

A;Reference number: A59328

C;Genetics:

A;Gene: XF1129

Query Match Score 100.0%; Score 21; DB 2; Length 54;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4

Db 50 YYAD 53

RESULT 4

PC222 GTP-binding protein rhoA - pig (fragment)

C;Species: *Sus scrofa domestica* (domestic pig)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000

C;Accession: PC4222

R;Nishimura, J.; Sakihi, C.; Zhou, Y.; Kanaike, H.

Biochem Biophys Res Commun 227, 750-754, 1996

A;Title: Expression of rho A and rho kinase mRNAs in porcine vascular smooth muscle.

A;Reference number: PC4222; MUID:97040692; PMID:9886005

A;Accession: PC4222

A;Molecule type: mRNA

A;Cross-references: DDBJ:DR9492; NID:91695730; PIDN:BA13966.1; PID:91695731

C;Comment: This protein is involved in the inhibition of myosin light chain phosphatase.

C;Genetics:

A;Gene: rhoA

C;Superfamily: ras transforming protein; translation elongation factor Tu homology

C;Keywords: GTP binding

Query Match Score 100.0%; Score 21; DB 2; Length 66;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4

Db 7 YYAD 10

RESULT 5
PC4266 GTP-binding protein rhoA - rat (fragment)

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 13-Aug-1999

C;Accession: PC4266

R;Nishimura, J.; Sakihara, C.; Nakano, H.; Kanaike, H.

Biochem Biophys Res Commun 230, 356-359, 1997

A;Title: Up-regulation of rho A and rho-kinase mRNAs in the rat myometrium during pregn

A;Reference number: PC4266; MUID:9016783

A;Accession: PC4266

A;Molecule type: mRNA

A;Cross-references: 1-66 <NII>

C;Comment: This protein is involved in the smooth muscle myofil

C;Keywords: GTP binding

Query Match Score 100.0%; Score 21; DB 2; Length 66;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4

Db 7 YYAD 10

RESULT 6
GB2969 probable transcription regulator PA5403 [Imported] - *Pseudomonas aeruginosa* (strain BAC

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: Q82969

R;Stoyer, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kes, A.; Larbig, K.; Lim

; Lory, S.; Olson, M.V.

Nature 406, 959-963, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path

A;Reference number: A82950; MUID:1038437; PMID:10984043

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA5403

Query Match Score 100.0%; Score 21; DB 2; Length 68;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4

Db 64 YYAD 67

RESULT 7
AC1251 hypothetical protein lml411 [Imported] - *Listeria monocytogenes* (strain EdD-e)

C;Species: *Listeria monocytogenes*

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001

C;Accession: AC1251

R;Glaser, P.; Prangual, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blooeck, H

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H

D.; Jones, L.M.; Karst, U.

Science 284, 849-851, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M

ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland

A;Title: Comparative Genomics of *Listeria* species

A;Reference number: AB1077; MUID:2153279; PMID:11679659

A;Accession: AC1251

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-75 <GLA>
 A;Cross-references: GB:NC_003210; RIDN: CAC99489_1; PID:916410840; GSPDB:GN00177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lm01411
 Query Match Similarity 100.0%; Score 21; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 65 YYAD 68

RESULT 8
 SFRA-C-6 Protein - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: S51629
 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
 R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaek, S.; Carlsson, P.
 EMBO J. 13, 5002-5012, 1994
 A;Title: Cloning and characterization of seven human forkhead proteins: binding site specificities; nucleic acid sequence not shown
 A;Reference number: S51624; MUID:9504532; PMID:7957066
 A;Accession: S51629
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-76 <PIB>
 A;Cross-references: ENBL:U13224; NID:9563167; PID:AA92041_1; PMID:9563168
 C;Genetics:
 A;Gene: GDB:FKH110; FREAC6
 A;Cross-references: GDB:450228; OMIM:601093
 A;Map position: 5q34-5q34
 C;Superfamily: unassigned fork head proteins_fork head DNA-binding domain homology (fragment) <FHD>
 F;6-76/Domain: fork head DNA-binding domain homology

Query Match Similarity 100.0%; Score 21; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 35 YYAD 38

RESULT 9
 R3B918 ribosomal protein S18 - *Bacillus stearothermophilus*
 C;Species: *Bacillus stearothermophilus*
 C;Accession: S03556
 R;McDougal, J.; Choli, T.; Kruft, V.; Kapp, U.; Witmann-Liebold, B.
 FEBS Lett. 245, 253-260, 1989
 A;Title: The complete amino acid sequence of ribosomal protein S18 from the moderate thermophile
 A;Reference number: S03556; MUID:89171319; PMID:2647521
 A;Accession: S03556
 A;Molecule type: protein
 A;Residues: 1-77 <MCD>
 C;Superfamily: *Escherichia coli* ribosomal protein S18
 C;Keywords: protein biosynthesis; ribosome

Query Match Similarity 100.0%; Score 21; DB 1; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 73 YYAD 76

RESULT 10
 AG1613 hypothetical protein lin1448 [imported] - *Listeria innocua* (strain Clip11262)
 C;Species: *Listeria innocua*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 R;Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloechl, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.;
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourna, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vaquerz-Boland, J.A.; Voss, H.; Wehlan, A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Status: preliminary
 A;Accession: AG1613
 A;Molecule type: DNA
 A;Residues: 1-80 <GLA>
 A;Cross-references: GB:AB592022; PIDN:CA956679_1; PID:916413921; GSPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin1448

Query Match Similarity 100.0%; Score 21; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 70 YYAD 73

RESULT 11
 I51103 Major Histocompatibility Complex class II B - ring-necked pheasant (fragment)
 C;Species: *Phasianus colchicus* (ring-necked pheasant)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
 C;Accession: I51103
 R;Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
 Immunogenetics 39, 395-403, 1994
 A;Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
 A;Reference number: I51103
 A;Accession: I51103
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-82 <WIT>
 A;Cross-references: EMBL:X75403; PIDN:CA53157_1; PID:9496921
 C;Superfamily: Class II histocompatibility antigen; immunoglobulin homology

Query Match Similarity 100.0%; Score 21; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 42 YYAD 45

RESULT 12
 I51106 Major Histocompatibility Complex class II B - ring-necked pheasant (fragment)
 C;Species: *Phasianus colchicus* (ring-necked pheasant)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
 C;Accession: I51106
 R;Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
 Immunogenetics 39, 395-403, 1994
 A;Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
 A;Reference number: I51103
 A;Accession: I51106
 A;Molecule type: DNA
 A;Residues: 1-62 <WIT>
 A;Cross-references: EMBL:X75406; PIDN:CA53160_1; PID:9496927
 C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Tue May 25 09:02:29 2004

Query Match Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 42 YVAD 45

RESULT 13
E71321 hypothetical protein TP0467 - syphilis spirochete
C;Species: Treponema pallium subsp. Pallidum (syphilis spirochete)
C;Date: 24-Jul-1995 #sequence_revision 24-Jul-1995 #text_change 05-Nov-1999
C;Accession: E71321
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rison, J.; Weilak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDaniel,
They, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-386, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: E71321
A;Status: Preliminary; nucleic acid sequence not shown;
A;Molecule type: DNA
A;Residues: 1-82 <COL>
A;Cross-references: GB:A001223; GB:NE000520; NID:93322745; PID:ANG65458.1; PID:9332275
A;Experimental source: strain Nichols
C;Genetics:

Query Match Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 31 YVAD 34

Qy 1 YVAD 4
Db 15 YVAD 18

RESULT 15
S71291 retrovirus-related reverse transcriptase homolog (clone Rrtat3) - Arabidopsis thaliana (
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Variety: strain Columbia
A;Variety: strain Columbia
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S71291
R;Brändes, A.; Heslop-Harrison, J.S.; Kamm, A.; Kubis, S.; Doudrick, R.L.; Schmidt, T.
submitted to the EMBL Data Library, January 1996
A;Description: Comparative analysis of the chromosomal and genomic organization of Ty1-
A;Reference number: S71291
A;Accession: S71291
A;Molecule type: DNA
A;Residues: 1-88 <BRA>
A;Cross-references: EMBL:268911; NID:gil171493; PIDN:CAA93146.1; PID:gil171494
C;Genetics:

Query Match Score 21; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
Db 20 YVAD 23

RESULT 14
A28033 GTP-binding protein rhoB - bovine (fragments)
N;Alternate name: 20K GTP-binding protein rho; rhoB* protein; transforming protein rhoB
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Aug-1995 #sequence_revision 05-Apr-1995 #text_change 13-Aug-1999
C;Accession: A28033; B28324; E60050
R;Yamamoto, K.; Kondo, J.; Hishida, T.; Teranishi, Y.; Takai, Y.
J. Biol. Chem. 263, 9926-9932, 1988
A;Title: Purification and characterization of a GTP-binding protein with a molecular weight
A;Reference number: A28033; MUID:88251127; PMID:3133371
A;Accession: A28033
A;Molecule type: protein
A;Residues: 1-33:48-53:59-71 <WIL>
A;Experimental source: brain
R;Hoshijima, M.; Kondo, J.; Kikuchi, A.; Yamamoto, K.; Takai, Y.
Brain Res. Mol. Brain Res. 7, 9-16, 1990
A;Title: Purification and characterization of soluble rho catalyzed by Clostridium
C1; identifier: A38324; MUID:91065876; PMID:2174426
A;Accession: B38324
A;Molecule type: protein
A;Residues: 1-33:48-53:59-71 <WIL>
A;Experimental source: brain
R;Hoshijima, M.; Kondo, J.; Kikuchi, A.; Yamamoto, K.; Vaughan, M.
Brain Res. Mol. Brain Res. 7, 9-16, 1990
A;Title: Purification and characterization of a GTP-binding protein from bovine brain membranes of a C1; identifier: A38324; MUID:91065876; PMID:2174426
A;Reference number: A60050; MUID:90135940; PMID:2153899
A;Accession: B60050
A;Molecule type: protein
A;Residues: 54-68:72-86 <HO2>
A;Experimental source: brain
C;Genetics:
A;Gene: rhoB

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OM Protein - Protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 10.5 Seconds
(without alignments)
19.836 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	32	1 ADHR_DROYA	P28487 drosophila
2	21	100.0	36	1 PAHO_RABBIT	P11336 oryctolagus
3	21	100.0	37	1 CTDP1_SARBU	P80504 solatin cub
4	21	100.0	43	1 CTDP1_DROME	P14485 sarcophaga
5	21	100.0	74	1 RS18_CHLTER	Q8ram3 chloroforium
6	21	100.0	75	1 HEI5_RHOPB	P80482 rhoferax
7	21	100.0	77	1 RS18_BACST	P10306 bacillus st
8	21	100.0	82	1 Y467_TREPA	P8480 treponema p
9	21	100.0	94	1 YCQV_BACSU	P51499 bacillus su
10	21	100.0	102	1 CPA1_CANPG	P81175 cancer pagu
11	21	100.0	104	1 CLP5_DROME	P92192 drosophila
12	21	100.0	105	1 CPA2_CANPG	P81576 cancer pagu
13	21	100.0	113	1 YF90_MYCTO	Q10168 mycobacteri
14	21	100.0	117	1 GHHA_ACALA	P30370 acanthopae
15	21	100.0	122	1 TVB5_MOUSE	P02123 mus musculu
16	21	100.0	125	1 C014_MENSE	P13229 manduca sex
17	21	100.0	126	1 CLP2_DROME	P91129 drosophila
18	21	100.0	138	1 C1P1_DROME	P91627 drosophila
19	21	100.0	143	1 CU17_BOMMO	Q02387 bombyx mori
20	21	100.0	152	1 ACM_DROME	Q94519 drosophila
21	21	100.0	156	1 C055_ARADI	P80518 araneus dia
22	21	100.0	159	1 C1U57_ARADI	P80519 araneus dia
23	21	100.0	159	1 OBPS_BOVIN	P07435 bos taurus
24	21	100.0	161	1 H221_MAIZE	P24631 zea mays (m
25	21	100.0	163	1 DRD_NEIMA	Q9jje7 neisseria m
26	21	100.0	171	1 Y011_NEVOP	O10301 orgyia pseu
27	21	100.0	174	1 AROK_STPAM	Q99e16 staphylococ
28	21	100.0	174	1 AROK_STPAM	O8rmc8 bombyx mori
29	21	100.0	174	1 CTG22_BOMMO	P02388 bombyx mori
30	21	100.0	180	1 CYSH_RHITR	O33579 rhizobium t
31	21	100.0	182	1 APT_PSPK	Q88133 pseudomonas
32	21	100.0	182	1 NODC_RHILT	P04678 rhizobium l
33	21	100.0	184	1 C0UP_DROME	P14384 drosophila

ALIGNMENTS

RESULT 1		ADHR_DROYA		STANDARD;		PRT;		32 AA.	
ID	ADHR_DROYA	ID	P28487;	AC	P28487; (Rel. 24, Created)	DT	01-DEC-1992 (Rel. 24, Last sequence update)	RHO_DISM	RHO DISM
AC	P28487;	AC	P28487;	DT	01-DEC-1992 (Rel. 24, Last sequence update)	GN	ADHR	RHO_CANFA	RHO CANFA
DT	01-DEC-1992 (Rel. 24, Last sequence update)	DT	01-OCT-1996 (Rel. 34, Last annotation update)	DE	Alcohol dehydrogenase related 31 kDa protein (Fragment).	OS	Drosophila yakuba (Fruit fly).	RHO_HUMAN	RHO HUMAN
DT	01-OCT-1996 (Rel. 34, Last annotation update)	GN	Drosophila yakuba (Fruit fly).	OS	Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Drosophilidae; Drosophila; Drosophila.	OC		RHO_MOUSE	RHO MOUSE
RA	Ashburner M.	RA	SEQUENCE FROM N.A.	NCBI_TAXID=7245;	RN [1]	RP	Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.	OX	
RL		RL			- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.	CC		CC	
CC		CC			This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC		CC	
CC		CC			DR EMBL; X51420; CRA3064.1; - .	DR		DR	
CC		CC			DR PIR; S20719; S20719.	DR		DR	
CC		CC			DR InterPro; P8gn012364; Dyak_Adr.	DR		DR	
CC		CC			DR PROSITE; PS00061; ADH_short.	DR		DR	
CC		CC			KW Oxidoreductase.	KW		KW	
CC		CC			PT NP_BIND 11 >32 NAD OR NADP (BY SIMILARITY).	PT		PT	
CC		CC			FT NON_TER 32 32 NAD OR NADP (BY SIMILARITY).	FT		FT	
CC		CC			SQ SEQUENCE 32 AA; 3412 MW; 9302949AFCB7D4F CRC64;	SQ		SQ	
CC		CC			Query Match Similarity 100.0%; Score 21; Length 32;				
CC		CC			Best Local Similarity 100.0%; Pred. No. 28; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
CC		CC			QY 1 YVAD 4	QY		QY	
CC		CC			Db 11 YVAD 14	Db		Db	

RESULT 2		PAHO_RABIT		STANDARD;		PRT;		36 AA.	
ID	P41376; (Rel. 31, Created)	ID	P41376; (Rel. 31, Last sequence update)	AC	P41376; (Rel. 31, Last sequence update)	DT	01-FEB-1995 (Rel. 31, Last sequence update)	RHO_DROME	RHO DROME
AC	P41376; (Rel. 31, Created)	AC	P41376; (Rel. 31, Last sequence update)	DT	01-FEB-1995 (Rel. 31, Last sequence update)	GN		RHO_CANFA	RHO CANFA
DT	01-FEB-1995 (Rel. 31, Last sequence update)	GN		DT	01-FEB-2003 (Rel. 42, Last annotation update)	OS	Pancreatic hormone (Pancreatic polypeptide).	RHO_MOUSE	RHO MOUSE
DT	01-FEB-2003 (Rel. 42, Last annotation update)	OS	Pancreatic hormone (Pancreatic polypeptide).	DB		DB		DB	

GN PPV
 OS Oryctolagus cuniculus (Rabbit); Craniata; Vertebrata; Euteleostomi;
 OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCB_TaxID=9386;
 RN [1]
 RP
 SEQUENCE
 TISSUE=Pancreas;
 MEDLINE=54136533; PubMed=8299350;
 RA Marks N.J., Shaw C., Halton D.W., Curry W.J., Thim L.;
 RT "Rabbit Pancreatic polypeptide";
 Comp. Biochem. Physiol. 108B:883-887(1992).
 -: FUNCTION: Pancreatic hormone is synthesised in pancreatic islets
 of Langherans and acts as a regulator of pancreatic and
 gastrointestinal functions.
 -: SUBCELLULAR LOCATION: Secreted.
 -: SIMILARITY: Belongs to the NPY family.
 DR HSSP; P01302; IBBA.
 InterPro; IP00195; Pancreatic_hormn.
 PFAM; PF00159; hormone3_1.
 PRINTS; PR00278; PANCHORMONE.
 SMART; SMO0309; PAH; 1.
 PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
 PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.
 Hormone; Amidase; Pancreas.
 MOD RES 36 amidation.
 SEQUENCE 36 AA; 4197 MW; A14A430831AT759D CRC64;
 Query Match Similarity 100.0%; Score 21; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy	YVAD 4	Ddb	20 YVAD 23

RESULT 3
 ATPO_SOTU ATPO_SOTU STANDARD; PRT; 37 AA.
 P80504; 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DBP synthase delta chain, mitochondrial (EC 3.6.3.14) (Oligomycin
 sensitivity conferral protein) (OSCP) (Fragment).
 DE Solanum tuberosum (Potato).
 OS Solanum tuberosum (Potato).
 OC Bivalvia; Viridiplanteae; Streptophytina; Embryophytina; Tracheophytina;
 OC Spermatophytina; Magnoliophyta; eudicots; core eudicots; asterids;
 OC Solanales; Solanaceae; Solanum.
 OX NCB_TaxID=4113;
 RN [1]
 RP
 SEQUENCE
 TISSUE=Tuber;
 MEDLINE=5707345; PubMed=8919912;
 RA Jarsch L., Kraut V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 of the protein complexes of plant mitochondria.";
 Plant J. 9:357-368(1996).
 -: FUNCTION: This protein seems to be part of the stalk that links
 CF(0) to CF(1). It either transmits conformational changes from
 CF(0) into CF(1) or is implicated in proton conduction.
 -: CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
 H(+)(Out).
 -: SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
 core - and CF(0) - the membrane proton channel. CF(1) has five
 subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
 has three main subunits: a, b and c.
 -: SUBCELLULAR LOCATION: Mitochondrial.
 -: SIMILARITY: Belongs to the ATPase delta chain family.
 InterPro; IPR000711; ATPsynT_OSCP.
 PROSITE; PS00389; ATPase_DELTA; PARTIAL.
 Hydrolase; ATP_synthase; CF(1); Hydrogen ion transport;

Mitochondrion.	FT	NON TER	37	37 AA;	4003 MW;	9BFDAB1A298F4AF CRC64;
SQ	SEQUENCE	37 AA;	4003 MW;	9BFDAB1A298F4AF CRC64;		
Query Match	Best Local Similarity	100.0%	Score 21;	DB 1;	Length 37;	
Matches 4;	Conservative	100.0%	Pred. No. 32;			
		0;	Mismatches 0;			Indels 0;
Qy:	1 YYAD 4					
Db:	8 YYAD 11					
RESULT 4						
CUP1_SARB	CUP1_SARB	STANDARD;	PRT;	43 AA.		
ID	ID					
AC	P14455;					
PP	01-JAN-1990 (Rel. 13, Created)					
RT	01-JAN-1990 (Rel. 13, Last sequence update)					
DT	28-FEB-2003 (Rel. 41, Last annotation update)					
DB	Larval cuticle protein S1 (Fragment).					
OS	Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata)					
OC	Neoptera; Endopterygota; Hexapoda; Insecta; Pterygo-					
OC	Neoptera; Endopterygota; Diptera; Brachycera; Musconorpha;					
OC	Sarcophagidae; Sarcophaga.					
OX						
RN						
RP						
SEQUENCE.						
RX	Medline=86037264; PubMed=39322663;					
RA	Henzel W.J., Mole J.E., Muligan K., Lipke H.;					
RT	"Sarcophaga" larval proteins: partial sequence homologies of cuticle proteins and related structures of drosophilids.";					
RL	J. Mol. Evol. 2:39-45(1985).					
CC	- - SIMILARITY: Component of the cuticle of the larva of file					
CC	PIR; A24553; A24553.					
DR	InterPro0616; Insect cuticle.					
DR	Pfam: PF00379; Chitin_bind_4; 1.					
DR	PROSITE: PS00233; CUTICLE; PARTIAL.					
KW	Structural protein; Cuticle.					
FT						
NON TER	43					
SQ	SEQUENCE	43 AA;	4556 MW;	6B3FD9A0B67E2210 CRC64;		
Query Match	Best Local Similarity	100.0%	Score 21;	DB 1;	Length 43;	
Matches 4;	Conservative	100.0%	Pred. No. 38;			
		0;	Mismatches 0;			Indels 0;
Qy:	1 YYAD 4					
Db:	39 YYAD 42					
RESULT 5						
RS18_ID	_RS18_CHLITE	STANDARD;	PRT;	74 AA.		
AC	Q8K4J3;					
PP	28-FEB-2003 (Rel. 41, Created)					
RT	28-FEB-2003 (Rel. 41, Last sequence update)					
DT	10-OCT-2003 (Rel. 42, Last annotation update)					
DB	30S ribosomal protein S18.					
GN	RPSR OR CT2133.					
OS	Chlorobium tepidum.					
OC	Chlorobi; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae					
OC	Chlorobium.					
OX						
RN						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=TLS / ATCC 49652 / DSM 12025;					
RX	Medline=21103685; PubMed=1203901;					
RA	Ensm J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu					
RA	Dodson R.J., DeBoy R., Gwinn M.L., Nelson W.C., Haft D.H.,					
RA	Hickey E.K., Peterson J.D., Durkin S.K., Kolonay J.L., Yan					
RA	Holt I.J., Umayam L.A., Mason T.P., Brenner M., Shatsky T.P., Par					
NCBI_TaxID	=1097;					

RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D., Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A., Ventler J.C., Tetelin H., Bryant D.A., Fraser C.M.; "The complete genome of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium"; Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
 CC -!- SUBUNIT: Binds as a heterodimer with protein S6 to the central domain of the 16S rRNA, where it helps stabilize the platform of the 30S subunit (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight heterodimer with protein S5 (By similarity).
 CC -!- SIMILARITY: Belongs to the S18P family of ribosomal proteins.
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 CC EMBL: AE012662; AAM73349.1; - .
 DR TIGR; CT2133; .
 DR HAMAP; MF_00270; - .
 DR InterPro; IPR001648; Ribosomal S18; .
 DR PFAM; PF01684; Ribosomal S18; .
 DR PRINTS; PR00974; RIBOSOMAL S18; .
 DR PRODOM; PD002239; Ribosomal S18; .
 DR TIGRFAMS; TIGR00165; S18; .
 DR PROSITE; PS00057; RIBOSOMAL S18; FALSE_NEG.
 DR RIBOSMAL Protein; RNA-binding; rRNA-binding; Complete proteome.
 KW SEQUENCE 74 AA; 8671 MW; 7120CA25284DB8B CRC64;
 SQ 100.0%; Score 21; DB 1; Length 74;
 Best Local Similarity 100.0%; Pred. No. 65; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 68 YYAD 71

RESULT 6
 HP-1S_RHOFE ID RHOFE STANDARD; PRT; 75 AA.
 AC P08882;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE High potential iron-sulfur protein (HipIP).
 GN HIP.
 CC Rhodofrax fermentans.
 CC Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Comamonadaceae; Rhodobacter.
 OX NCBI_TaxID=280666;
 RN 1
 RP SEQUENCE.
 RX MEDLINE=97344565; PubMed=9119002;
 RA van Driesche G., Ciurli S., Hochkoeppler A., van Beumen J.J.; "The primary structure of Rhodofrax fermentans high-potential iron-sulfur protein, an electron donor to the photosynthetic reaction center"; Eur. J. Biochem. 244:371-377 (1997).
 CC -!- FUNCTION: Specific class of high-redox-potential 4Fe-4S ferredoxins. Functions in anaerobic electron transport in most purple and in some other photosynthetic bacteria and in at least one genus (Paracoccus) of halophilic, denitrifying bacteria.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: Belongs to the high potential iron-sulfur protein (HipIP) family.
 CC HSSP; P00260; 1CKU.

DR InterPro; IPR000170; Hipot_ironsulf.
 DR Pfam; PF01355; HIP1P; 1.
 DR PROSITE; PS00596; HIP1P; 1.
 KW IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 FT METAL 38 38 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 FT METAL 41 41 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 FT METAL 54 54 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 FT METAL 68 68 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).
 SQ SEQUENCE 75 AA; 7849 MW; 9F6C86B662A72D3 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 75;
 Best Local Similarity 100.0%; Pred. No. 66; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 17 YYAD 20

RESULT 7
 RS18_BACST ID RS18_BACST STANDARD; PRT; 77 AA.
 AC P10816;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB 30S ribosomal protein S18 (RS18) (RS18).
 GN RPSR.
 OS Bacillus stearothermophilus
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus
 OC NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=799;
 RX MEDLINE=89171319; PubMed=2647521;
 RA McDougall J., Choi I.T., Krut V., Kapp U., Wittmann-Liebold B.; "The complete amino acid sequence of ribosomal Protein S18 from the moderate thermophile Bacillus stearothermophilus"; FEBS Lett. 245:253-260(1989).
 RL [2]
 RN PIR: S03556; R3BS18.
 RP SEQUENCE OF 1-15.
 RC STRAIN=10;
 RX MEDLINE=75019590; PubMed=4607606;
 RA Yaguchi M., Matheson A.T., Visentini L.P.; "Prokaryotic ribosomal proteins: N-terminal sequence homologies and structural correspondence of 30 S ribosomal proteins from Escherichia coli and Bacillus stearothermophilus"; FEBS Lett. 46:1296-300(1974).
 CC -!- FUNCTION: Binds as a heterodimer with protein S6 to the central domain of the 16S rRNA, where it helps stabilize the platform of the 30S subunit (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight heterodimer with protein S6 (By similarity).
 CC -!- SIMILARITY: Belongs to the S18P family of ribosomal proteins.
 DR PIR: S03556; R3BS18.
 DR HAMAP; MF_00270; - .
 DR InterPro; IPR001648; Ribosomal S18.
 DR Pfam; PF01084; Ribosomal S18; 1.
 DR PRINTS; PR00974; RIBOSOMAL S18; 1.
 DR PRODOM; PD00239; Ribosomal S18; 1.
 DR TIGRFAMS; TIGR00165; S18; 1.
 DR PROSITE; PS00057; RIBOSOMAL S18; 1.
 DR Ribosomal Protein; RNA-binding; rRNA-binding.
 FT INIT_MET 0 0
 SQ SEQUENCE 77 AA; 8837 MW; A3F635FC64210E42 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 77;
 Best Local Similarity 100.0%; Pred. No. 68; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 73 YYAD 76

RESULT 8
 Y467_TREPA STANDARD; PRT; 82 AA.
 AC OS3480;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein TP0467.
 GN TP0467.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N.A.;
 STRAINNICKNAME;
 RX MEDLINE=98322770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Kerlach K.A.,
 RA Sodergren R., Hardham J.M., McNeil M.P., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.,
 PT "Complete genome sequence of *Treponema pallidum*, the syphilis
 RT spirochete." Science 281:375-388 (1998).
 RL

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DR EMBL; AE001233; AAC65458..1; -.
 DR PIR; ET1321; ET1321.
 DR TIGR; TP0467; .
 KW Hypothetical Protein; Complete Proteome;
 SQ SEQUENCE 82 AA; 9614 MW; PDBA0CBE370890C CRC64; .
 Query Match 100.0%; Score 21; DB 1; Length 92;
 Best Local Similarity 100.0%; Fred. No. 72;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 31 YVAD 34

RESULT 9
 YQGV_BACSU STANDARD; PRT; 94 AA.
 AC P54459;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein yqgv.
 GN YQGV OR SSU24810.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBITaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16B / JH642;
 RX MEDLINE=97124195; PubMed=8969508;
 RA Mizuno M., Masuda S., Takeuchi M., Hosono S., Sato T., Takeuchi M.,
 RA Kobayashi Y.;
 RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
 RT the *Bacillus subtilis* genome containing the *spa* element and many
 RT sporulation genes.";

RL Microbiology 142:3103-3111(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16B;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogawa N., Moszer I., Albertini A.M., Alloni G., Bolognini A., Borchert S.,
 RA Azzevedo V., Bertone M.G., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Borrius R., Bourrier L., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabre C., Ferrari E., Fouger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G., Guiseppi G., Guy B.J., Hales J., Harwood C.R., Heaut A., Hillert H., Hollaspeel S., Hosono S., Hull J., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaeser-Blanchard M., Klein C., Kubiyashiki Y., Koetter P., Koningsstein G., Krogh S., Kurita K., Lapidus A., Lardinois S., Labey J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado P., Mizuno M., Moestl D., Nakai S., Noback M., Medina D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portereit D., Porwollik S., Prescott A.M., Presecan E., Puigc P., Pur nelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rocic M., Sadie Y., Sato T., Scanlan E., Schleicher S., Schroeter R., Scuffene F., Sorokin A., Taccioni B., Takagi T., Takahashi H., Takekamu K., Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Tognoni A., Tosato V., Uchiyama S., Vandembol M., Vanner F., Vassarotti A., Vizari A., Wambutt R., Wedler B., Wedler H., Weitznerger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yata K., Yoshida K., Yoshioka H.F., Zumstein E., Yoshikawa H., Danchin A.; subtilis ;
 RT Nature 390:249-256(1997).
 CC --! SIMILARITY: BELONGS TO THE UPF0045 FAMILY.

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DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR Sublist: BG11689; yqgv.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; D84432; BAA1525.1; -.
 DR PIR; G69957; G69957.
 DR DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
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 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
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 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
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 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
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 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
 DR EMBL; Z99116; CAB14142.1; -.
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 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
 SQ SEQUENCE 94 AA; 10453 MW; 4A576F233B880999 CRC64;
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 DR InterPro; IPR002767; DUFT7.
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 KW Hypothetical Protein; Complete proteome
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 DR EMBL; Z99116; CAB14142.1; -.
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 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
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 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
 KW Hypothetical Protein; Complete proteome
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 DR PFam; PF01310; DUFT7; 1.
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 DR PFam; PF01310; DUFT7; 1.
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 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
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 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
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 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
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 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.
 DR PFam; PF01310; DUFT7; 1.
 DR TIGRFAMS; TIGR00106; TIGR00106; 1.
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 DR EMBL; Z99116; CAB14142.1; -.
 DR PIR; G69957; G69957.
 DR InterPro; IPR002767; DUFT7.

Cancer pagurus (Rock crab).
 OC Bukaryota; Metazoa; Crustacea; Malacostraca;
 OC Eumalacostraca; Decapoda; Palaemonida; Brachyura;
 OC Subbrachyura; Cancroidea; Cancridae; Cancer.
 OX NCBI_TaxID:6755;

[1] RN
 RP SEQUENCE.
 RC TISSUE-Carapace cuticle;
 RX MEDLINE=93154472; PubMed=10425740;

[2] RA Benoit K.Y., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borckova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke T.J., Davies P.,
 RA de Pablo B., Delicher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evguenieva C.C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabriele A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Illegram C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kerchuk K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kolip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.-H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Moskrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Neilson D.R., Neilson K.A., Nixon K., Nuissier D.R., Paclob J.M.,
 RA Palizzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M.M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbachach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.-A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.-H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).

[3] RN [4]

RESULT 11

LCPS_DROME
 ID LCPS_DROME STANDARD;
 AC P92132; OV69305;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

[5] DR "Last annotation update"

[6] DR Larval cuticle protein V precursor.
 GN (LCP65AB1 OR LCP5 OR DCP3 ALPHA OR CG18776) AND
 GN (LCP65AB2 OR LCP5 OR DCP3-BETA OR CG18773).

[7] OS Drosophila melanogaster (Pruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.

[8] DR TAXID=7277;

[9] RN SEQUENCE FROM N.A.

[10] RC STRAIN=Oregon-R;
 RA Mandalapati P., Jiang S., Schneider G., Chihara C.;
 RT "The cuticle proteins of *Drosophila melanogaster*: sequence of Lcps in
 the third chromosome cluster";
 RL Dros. Info. Service 77:49-51 (1996).

[11] RN SEQUENCE FROM N.A.

[12] RC STRAIN=Berkeley;
 RX MEDLINE=98013412; PubMed=9383044;

[13] RA Charles J.-P., Chihara C., Nejedl S., Riddiford L.M.,
 RT "A cluster of cuticle genes of *Drosophila* at 65A: sequence, structure
 and evolution";
 RT Genetics 147:1213-1224 (1997).

[14] RN SEQUENCE FROM N.A.

[15] RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;

[16] RA Adams M.D., Celtniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Chmpne M., Pfaffler B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

FT CONFLICT 62 72 AA; AAIVTGSETKVV>CRCBRBRILHUG (IN REF. 1).
 SQ SEQUENCE 104 AA; 11267 MW; BA60DD9483DD692 CRC64;
 Query Match Score 21; DB 1; Length 104;
 Best Local Similarity 100.0%; Fred. No. 92;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 84 YVAD 87

RESULT 12
 CPA2_CANPG STANDARD; PRT; 105 AA.
 ID CPA2_CANPG
 AC P81576;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR Curcicle protein AM1159 (CPAM1159).
 OS Cancer pagurus (Rock crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Bivalvia; Brachyura; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Eucarida; Cancroidea; Cancridae; Cancer.
 RN 6755;
 RP SEQUENCE_Carapace cuticle;
 RX MEDLINE-99334472; PubMed=104255740;
 RA Andersen S.O.;
 RT "Exoskeletal Proteins from the crab, *Cancer pagurus*,";
 RL Comp. Biochem. Physiol. 123A:203-211(1999).
 CC -!- TISSUE_SPECIFICITY: Articular membrane.
 CC -!- MASS_SPECTROMETRY: MW=158.8; METHOD=MAIDI.
 CC -!- SIMILARITY: Contains 1 cuticle consensus domain.
 DR InterPro; IPR000618; Insect cuticle.
 DR PRINTS; PRO00547; Chitin bind_4; 1.
 DR PROSITE; PS00233; CUTICLE.
 KW STRUCTURAL PROTEIN; Cuticle; 1.
 SQ SEQUENCE 105 AA; 11586 MW; 6C8B27FA44E149729 CRC64;

Query Match Score 21; DB 1; Length 105;
 Best Local Similarity 100.0%; Fred. No. 93;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 63 YVAD 66

RESULT 13
 YJ90_MYCTU STANDARD; PRT; 113 AA.
 ID YJ90_MYCTU
 AC Q10868;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein Rv1990c/Mtb2044/Mtb2012C precursor.
 GN Rv1990c OR Mt2044 OR MtCY39.29 OR MB2012C.
 OS Mycobacterium tuberculosis, and
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773, 1765;

Qy SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 RN SEQUENCE FROM N.A.
 RP SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 RC SPECIES=M.borisi; STRAIN=AF2122/97;
 RX MEDLINE=22206494; PubMed=12218016;
 RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermoljeva M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.,
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence,"
 RT laboratory strains";
 RL J. Bacteriol. 184:5479-5490 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.borisi; STRAIN=AF2122/97;
 RX MEDLINE=22206494; PubMed=12218016;
 RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Prior M., Duboy S., Grondin S., Lacroix C., Monsempé C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Kestigian L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
 RT "The complete genome sequence of *Mycobacterium bovis*."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC

DR Z74125; CAA93394.1; -.
 DR EMBL; AE007056; AAC46320.1; -.
 DR EMBL; BX248341; CA996865.1; -.
 DR PIR; D70757; D70757.
 DR TIGR; MT2044; -.
 DR MTB2044; -.
 DR TubercuList; Rv1990c; -.
 DR SIGNAL_1_13; HYPOTHETICAL PROTEIN.
 FT CHAIN_14_113; HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 113 AA; 12488 MW; 41978DIBEA5E74C9 CRC64;

Query Match Score 21; DB 1; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4
 Db 58 YVAD 61

RESULT 14
 GLHA_ACALA STANDARD; PRT; 117 AA.
 ID GLHA_ACALA
 AC P30970;
 DT 01-JUL-1993 (Rel. 25, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Glycoprotein hormone alpha chain precursor (Gonadotropin alpha
 chain) (GTH-alpha).
 DE Acanthopagrus latipes (Yellowfin Porgy).
 OS Acanthopagrus latipes; Bacteria; Eutelostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
 OC Sparidae; Acanthopagrus.

NCBI_TaxID=8177;
 RN [1] SEQUENCE FROM N.A.
 RP Tsai H.J., Chen Y.L.,
 RA Submitted (XXXX-1992) to the EMBL/GenBank/DDBJ databases.
 RL -!
 CC -! SUBCELLULAR LOCATION: Secreted.
 CC -! Heterodimer of an alpha and a beta chain.
 CC -!
 CC -! SIMILARITY: Belongs to the Glycoprotein hormones alpha chain
 family.
 CC -!
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 CC or send an email to license@isab-sib.ch).
 CC -!
 DR EMBL; M9438; AAA48513.1; -.
 DR HSSP; P01215; 1XUL.
 DR InterPro; IPR00200; GF_cysknot.
 DR InterPro; IPR00476; Glyco_hormone.
 DR PFam; PF00236; hormone6; 1.
 DR PRINTS; PR00438; GPCYSKNOT.
 DR PRODOM; PRO02047; GLYCOPHORMONE_1.
 DR SMART; SM00067; GHA_1.
 DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
 DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
 DR PROSITE; PS50277; GLYCO_HORMONE_ALPHA_3; 1.
 KW Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 117 GLYCOPROTEIN_HORMONES_ALPHA_CHAIN.
 FT DISULFID 34 57 BY SIMILARITY.
 FT DISULFID 37 86 BY SIMILARITY.
 FT DISULFID 54 107 BY SIMILARITY.
 FT DISULFID 58 109 BY SIMILARITY.
 FT DISULFID 65 112 BY SIMILARITY.
 FT CARBOXYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOXYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 117 AA; 13061 MW; P9ACE213DB67AF14 CRC4;

Query Match 100.0% Score 21; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Missmatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 58 YYAD 61

RESULT 15
 TYB5_MOUSE STANDARD PRT; 122 AA.
 ID _TYB5_MOUSE
 AC P04213;
 DT 20-MAR-1987 [Rel. 04, Created]
 DT 20-MAR-1987 [Rel. 04, Last sequence update]
 DT 10-OCT-2003 [Rel. 42, Last annotation update]
 DB T-cell receptor beta chain V region C5 precursor (Fragment).
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuS.
 OX NCBI_TaxID10090;
 RN
 RX SEQUENCE FROM N.A.
 RX MEDLINE=8503663; PubMed=6092364;
 RA Patten P., Yokota T., Rohrbard J., Chien Y., Arai K., Davis M.M.;
 RT "Structure, expression, and divergence of T-cell receptor beta-chain
 RT variable regions.";
 RL Nature 312:40-46 (1984).
 CC -! MISCELLANEOUS: This sequence was derived from a T-helper clone.
 DR PIR; A02008; RWN5C5.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 36.5 Seconds
(without alignments)
34.577 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YFAD 4

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

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sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriaph:*

sp_archeap:*

SPREMBI_25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mc:*

sp_organelle:*

sp_phage:*

sp_plant:*

sp_rabbit:*

sp_virus:*

```

0; Gaps ; Indels 0; Mismatches 0;保守性比对 4; 匹配 4
QY 1 YVAD 4
DB 11 YVAD 14

RESULT 2
PBJM4 PRELIMINARY; PRT; 44 AA.
Q8BJM4 PRELIMINARY; PRT; 44 AA.
O8BJM4_23_Created (TREMBLrel. 23, Created)
O1-MAR-2003 (TREMBLrel. 23, Last sequence update)
O1-MAR-2003 (TREMBLrel. 25, Last annotation update)
O1-MAR-2003 (TREMBLrel. 25, Last annotation update)
Protein kinase C-like 2 (Fragment).
60343CCORK.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
PBJM4 TISSUE=Body; STRAIN=C57BL/6J; PubMed=2466851;
MEDLINE=22354683;
The PATROM Consortium.
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse genome transcriptome based on functional annotation of
60,770 full-length cDNAs";
Nature 40:563-573 (2002).
EMBL; AX082931; BAC38639.1;
MCD; MGI:1923929; 6030436CCORK;
GO; GO:0005324; P:ATP binding; IEA.
GO; GO:0004674; P:Protein serine/threonine kinase activity; IEA.
GO; GO:0006168; P:Protein amino acid phosphorylation; IEA.
InterPro; IPR00061; Kinase_C.
Pfam; PF00433; protein_C; I.
NON_TER 1 1
SEQUENCE 44 AA; 5277 MW; FP86B72F23FF8AB2 CRC64;

Query Match 100.0%; Score 21; DB 71; Length 44;
Best Local Similarity 100.0%; Pred. No. 2 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 39 YVAD 42

RESULT 3
Q858A7 PRELIMINARY; PRT; 45 AA.
Q858A7_24_Created (TREMBLrel. 24, Created)
O1-JUN-2003 (TREMBLrel. 24, Last sequence update)
O1-JUN-2003 (TREMBLrel. 24, Last annotation update)
Gp4.
Mycobacteriophage CJW1.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205869;
SEQUENCE FROM N.A.
MEDLINE=22592560; PubMed=12705866;
Pedilla_M.L., Ford_M.E., Houtz_J.M., Karthikeyan_T., Wadsworth_C.,
A Pedilla_M.L., Jacobs_Sera_D., Falbo_J., Gross_J., Pannunzio_N.R., ,
A Brucker_W., Kumar_V., Kandasamy_J., Keenan_L., Bardarov_S., ,
A Kriakov_J., Lawrence_J.G., Jacobs_W.R., Jr., Hendrix_R.W., ,
A Hartill_G.P., "Origins of highly mosaic mycobacteriophage genomes.", ,
A Cell 113:171-182 (2003).
L EMBL; AY129331; AAR01619; -
SEQUENCE 45 AA; 5310 MW; DDE0738293591F73 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 45;

```

PT	NON_TER	52 AA;	52 MW;	D5405D4025C11698 CRC64;	
SQ	SEQUENCE	52 AA;	6198 MW;	D5405D4025C11698 CRC64;	
Query Match	Best Local Similarity	100.0%;	Score 21; DB 7; Length 52;		
	Matches 4;	Conservative 0;	Pred. No. 3.3e+02;		
	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1 YYAD 4				
Db	24 YYAD 27				
RESULT 6					
Q31337	PRELIMINARY;	PRT;	52 AA.		
AC	Q31337;				
DT	01-NOV-1996 (TRMBLrel. 01, Created)				
DT	01-JUN-2003 (TRMBLrel. 24, Last annotation update)				
D3	MHC CLASS II B.				
GN	MHC CLASS II B.				
OS	Alligator mississippiensis (American alligator).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Crocodylia; Alligatorinae; Alligator.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=American alligator; TISSUE=Blood;				
RX	MEDLINE=96137171; PubMed=156410;				
RA	Edwards S.V., Grahn M., Potts W.K.;				
RT	"Dynamics of Mhc evolution in birds and crocodilians: amplification of class II genes with degenerate primers.",				
RT	Mol. Ecol. 4: 719-729(1995).				
RL	U24404;				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0044012; F:MHC Class II receptor activity; IEA.				
DR	GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.				
DR	GO; GO:0019886; P:antigen processing, exogenous antigen via M. . . ; IEA.				
DR	InterPro; IPR000353; MHC II beta.				
DR	Prfam; PF00969; MHC II beta; 1.				
DR	ProDom; PD000328; MHC II beta; 1.				
KW	Glycoprotein; MHC II; Transmembrane.				
FT	NON_TER	1	1		
FT	NON_TER	52	52 MW;	DB4EBDA025C11698 CRC64;	
SQ	SEQUENCE	52 AA;	6198 MW;	D5405D4025C11698 CRC64;	
Query Match	Best Local Similarity	100.0%;	Score 21; DB 7; Length 52;		
	Matches 4;	Conservative 0;	Pred. No. 3.3e+02;		
	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1 YYAD 4				
Db	24 YYAD 27				
RESULT 6					
Q31337	PRELIMINARY;	PRT;	52 AA.		
ID	Q31337;				
DT	01-NOV-1996 (TRMBLrel. 01, Created)				
DT	01-JUN-2003 (TRMBLrel. 24, Last annotation update)				
DB	MHC CLASS II antigen B (fragment).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Charadriiformes; Colopacidae;				
OC	Gallinago; Gallinago; Gallinago-Almeida S.; Vettore A.L.,				
OX	NCBI_TaxID=114734;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Game 6;				
RA	Ekblom R., Grahn M., Hoglund J.;				
RT	"Patterns of polymorphism in the MHC class II of a non-passerine bird, the great snipe (Gallinago media)."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.				
RL	EMBL; AF085412; AAL93175.1;				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0045012; F:MHC Class II receptor activity; IEA.				
DR	GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.				
DR	GO; GO:0006955; P:immune response, exogenous antigen via M. . . ; IEA.				
DR	InterPro; IPR000353; MHC II beta.				
DR	Prfam; PF00969; MHC II beta; 1.				
DR	ProDom; PD000328; MHC II beta; 1.				
KW	Glycoprotein; MHC II; Transmembrane.				
FT	NON_TER	1	1		
FT	NON_TER	53	53 MW;	P8AOBEE3C316727 CRC64;	
SQ	SEQUENCE	53 AA;	6235 MW;	P8AOBEE3C316727 CRC64;	
Query Match	Best Local Similarity	100.0%;	Score 21; DB 7; Length 53;		
	Matches 4;	Conservative 0;	Pred. No. 3.4e+02;		
	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1 YYAD 4				
Db	26 YYAD 29				
RESULT 8					
Q9PE99	PRELIMINARY;	PRT;	54 AA.		
ID	Q9PE99;				
AC	Q9PE99;				
DT	01-OCT-2000 (TRMBLrel. 15, Created)				
DT	01-OCT-2000 (TRMBLrel. 15, Last sequence update)				
DT	01-JUN-2003 (TRMBLrel. 24, Last annotation update)				
DS	Hypothetical protein XFL129.				
GN	XFL129.				
OS	Xylella fastidiosa.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaceae;				
OC	Xanthomonadaceae;				
NCBI_TaxID=2371;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=9ASC;				
RX	MEDLINE=20365717; PubMed=10910347;				
RA	Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aencio M., Alvaranga R., Alves L.M.C., Baptista C.S., Barros M.H., Bonacorsini E.D., Bordim S., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrasco D.M., Carrer H., Courinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Lopes N.B., Costa M.C.R., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho R., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franco S.C., Franco M.C.H., Furtan L.R., Garnier M., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuranda B.E., Laibert P., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Machado J.A., Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marinho C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhari A., Jr., Nobrega F.G., Nunes J.R., Oliveira M.P., Oliveira M.C., de Oliveira M.C., Oliveira R.C., Palmeri D.A., Paris A., Peixoto B.R., Pereira H.A., Pereira H.A., Jr., Pescquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., da Silva W.A., Jr., de Souza A.A., da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terzani M.F., Truffi D., Tezzi S.M., Tsuhako M.H., Valada H., van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zagó M.A., Zatz M., Meidanis J., Setubal J.C., "The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> ."; DR	EMBL; AE003949; AF83939; -;			
RA	PIR; H82718; H82718.				

KW Hypothetical protein; Complete proteome;
 SQ SEQUENCE 54 AA; FB7B7C4B250C4B7 CRC64;
 Query Match 100.0%; Score 21; DB 16; Length 54;
 Best Local Similarity 100.0%; Fred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVAD 4
 Db 50 YVAD 53

RESULT 9
 Q8Y145 PRELIMINARY; PRT; 62 AA.
 ID Q8Y145; AC Q8Y145; DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE RSP0548 OR RS06110.
 OS *Ralstonia solanacearum* (*Pseudomonas solanacearum*).
 OC Burkholderiaceae; Betaproteobacteria; Burkholderiales;
 OC *Burkholderia*; *Proteobacteria*; *Betaproteobacteria*; *Burkholderiales*.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Arlat M., Billault A., Brortier P., Artiguenave F., Gouzy J., Mangenot S.,
 RA Chandler M., Choisne N., Claude-Renaud C., Cattolico L.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:497-502(2002).
 DR EMBL: AL646061; CAD1450_1; -
 KW Hypothetical protein; Complete proteome;
 SQ SEQUENCE 62 AA; 6788 MW;
 3AAC89CAC50144F3 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 62;
 Best Local Similarity 100.0%; Fred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YVAD 4
 Db 46 YVAD 49

RESULT 10
 Q8XSA4 PRELIMINARY; PRT; 62 AA.
 ID Q8XSA4; AC Q8XSA4; DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Hypothetical protein RSP0574.
 GN RSP0574 OR RS06111.
 OS *Ralstonia solanacearum* (*Pseudomonas solanacearum*).
 OC Burkholderiaceae; Betaproteobacteria; Burkholderiales;
 OC *Burkholderia*; *Proteobacteria*; *Betaproteobacteria*; *Burkholderiales*.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brortier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisne N., Claude-Renaud C., Grebe T.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,

DR GO; GO:0008658; P: penicillin binding; IEA.
 DR GO; GO:00273; P: cell wall biosynthesis (sensu Bacteria); IEA.
 DR InterPro; IPR01460; Transpeptidase.
 DR Pfam; PF00905; Transpeptidase; 1.
 FT NON-TER 1
 FT NON-TER 1
 SQ SEQUENCE 66 AA; 7089 MW; 673DA1BCEC74B980 CRC64;
 Query Match 100.0%; Score 21; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 8 YYAD 11

RESULT 13
 ID P79275; PRELIMINARY; PRT; 66 AA.
 AC P79275; 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Rho A (Fragment).
 OS Sus scrofa (Pig).
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID:9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=domestic; TISSUE=pulmonary vein;
 RX MEDLINE=9704069; PubMed=886605;
 RA Nishimura J., Saitoh C., Zhou Y., Kanaike H.;
 RT "Expression of Rho A and Rho-Kinase mRNAs in Porcine Vascular Smooth
 Muscle"; Biochem. Biophys. Res. Commun. 227:750-754 (1996).
 RL EMBL; D89499; BAA1396.1; -.
 DR PIR; PC4222; PC4222.
 DR HSSP; P0674; 1FTN.
 DR GO; GO:0005525; P:GTP binding IEA.
 DR GO; GO:0005925; P:small monomeric GTPase activity; IEA.
 DR GO; GO:0027264; P:small monomeric GTPase mediated signal transduction; IEA.
 DR InterPro; IPR001806; Ras_transferring.
 DR Pfam; PF00011; ras; 1.
 KW GTP-binding.
 FT NON-TER 1
 FT NON-TER 66
 SQ SEQUENCE 66 AA; 7562 MW; 3BC71B220AD67C30 CRC64;

Query Match 100.0%; Score 21; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4
 Db 7 YYAD 10

RESULT 14
 ID Q8SP36; PRELIMINARY; PRT; 66 AA.
 AC Q8SP36; 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN PYPA1.10.
 OS Pygoscelsis papua (Gento Penguin).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;
 OC Pygoscelsis.
 OC NCBI_TaxID:30457;

RN [1]
 SEQUENCE FROM N.A. PubMed=11797106;
 RX MEDLINE=21655119;
 RA Tsuda T.T., Tauda M., Naruse T., Kawata H., Ando A., Shiina T.,
 RA Fukuda M., Kurita M., Lemaho I., Kuleski J.K., Inoko H.;
 RT "Phylogenetic analysis of Penguin (Spheniscidae) species based on
 RT sequence variation in MHC class II genes";
 RL Immunogenetics 53:712-716 (2001).
 DR EMBL; AB04359; BAB8630.1;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0045012; P: MHC Class II receptor activity; IEA.
 DR GO; GO:0019884; P: antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P: antigen processing, exogenous antigen via M. . . ; IEA.
 DR GO; GO:0006955; P: immune response; IEA.
 DR InterPro; IPR00328; MHC II beta; 1.
 DR Pfam; PF00969; MHC II beta; 1.
 DR ProDom; PD000328; MHC-II beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON-TER 66
 SQ SEQUENCE 66 AA; 7774 MW; A955PF9736710EADF CRC64;
 Query Match 100.0%; Score 21; DB 7; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4
 Db 29 YYAD 32

RESULT 15
 ID Q8SP52; PRELIMINARY; PRT; 66 AA.
 AC Q8SP52; 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DR Major histocompatibility complex (Fragment).
 GN PYANU.OL.
 OS Pygoscelis antarctica (Chinstrap penguin).
 OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrates; Buteleostomi;
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;
 OC Pygoscelis.
 OC NCBI_TaxID=79643;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=11797106;
 RX MEDLINE=21655119;
 RA Tsuda T.T., Tauda M., Naruse T., Kawata H., Ando A., Shiina T.,
 RA Fukuda M., Kurita M., Lemaho I., Kuleski J.K., Inoko H.;
 RT "Phylogenetic analysis of Penguin (Spheniscidae) species based on
 RT sequence variation in MHC class II genes";
 RL Immunogenetics 53:712-716 (2001).
 DR EMBL; AB043556; BAB86820.1;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0045012; P: MHC Class II receptor activity; IEA.
 DR GO; GO:0019884; P: antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P: antigen processing, exogenous antigen via M. . . ; IEA.
 DR InterPro; IPR000333; MHC II beta.
 DR Pfam; PF00969; MHC-II beta; 1.
 DR ProDom; PD000328; MHC-II beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON-TER 66
 SQ SEQUENCE 66 AA; 7839 MW; 841AD0CB0029FDC7 CRC64;
 Query Match 100.0%; Score 21; DB 7; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YYAD 4

Db 29 YVAD 32
Search completed: May 24, 2004, 14:41:00
Job time : 38.5 secs

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OM protein - protein Search, using SW mode!

Run on: May 24, 2004, 14:36:17 ; Search time 51 Seconds
 (without alignments)
 22.161 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: DDEV 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: GeneseqP1980s:*

2: GeneseqP2000s:*

3: GeneseqP2001s:*

4: GeneseqP2002s:*

5: GeneseqP2003as:*

6: GeneseqP2003bs:*

7: GeneseqP2003ds:*

8: GeneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4	Aaw06250 ICE peptide
2	21	100.0	4	Aaw76200 Mouse caspase
3	21	100.0	4	Aaw52756 Aminomech
4	21	100.0	4	Aaw8940 Apopain
5	21	100.0	4	Aaw56305 Peptide C
6	21	100.0	4	Aaw18948 Apopain
7	21	100.0	4	Aay15622 Peptide U
8	21	100.0	4	Aay04114 Enzyme co
9	21	100.0	4	Aaw68554 Apopain a
10	21	100.0	4	Aay4411 Caspase P
11	21	100.0	4	Aaw99676 Caspase R
12	21	100.0	4	Aaw994093 Pro tease
13	21	100.0	4	Aay78347 Caspase 1
14	21	100.0	4	Aay769646 Caspase 1
15	21	100.0	4	Aay99958 Tetraptapeptid
16	21	100.0	4	Aab22889 Caspase 3
17	21	100.0	4	Aay19940 Synthetic
18	21	100.0	4	Aay19040 Caspase 1
19	21	100.0	4	Aay88373 Peptide U
20	21	100.0	4	Aay83396 DEVD peptide
21	21	100.0	4	Aab226851 Synthetic
22	21	100.0	4	Aay80786 Fluorophore
23	21	100.0	4	Aao17431 Caspase 3
24	21	100.0	4	Aay65866 PARP cleavage
25	21	100.0	4	Aab10870 Aminocoumarin

ALIGNMENTS

RESULT 1	
ID	AAW06250 standard; peptide; 4 AA.
XX	
AC	AAW06250;
XX	
DT	03-MAR-1997 (first entry)
XX	
DE	ICE peptide substrate.
XX	
Mch2; Ced-3/Ice; cysteine protease; apoptosis; autoimmune disease; KW	cancer; HIV; Alzheimer's disease; therapy.
KW	
OS	Synthetic.
XX	
PN	WO9636698-A1.
XX	
PD	21-NOV-1996.
XX	
PF	16-MAY-1996; 96W0-US007010.
XX	
PR	18-MAY-1995; 95US-00446925.
XX	
PA	(UYJE-) UNIV JEFFERSON THOMAS.
XX	
PA	Litwack G, Alnemri ES, Fernandez-Alnemri T;
XX	
DR	WPI; 1997-012077/01.
XX	
PT	New isolated apoptotic cysteine protease, Mch 2 - used to develop prods. for use as anti-apoptotic agents or as cytotoxic agents.
XX	
PT	Disclosure; Page 28; 43BP; English.
PS	
CC	A tetrapeptide (AAW06250) represents a site present in poly(ADP-ribose) that is cleaved by an interleukin-1 beta converting enzyme (ICE)-like protein during apoptosis. Another tetrapeptide (AAW06453) is the ICE cleavage site in pro-interleukin-1 beta. The 2 peptides were used to test the activity of human Cop32, ICE and 2 isoforms alpha (see also AAW0644) and beta (AAW0645), of novel human apoptotic cysteine protease Mch2. Enzymatic activities were studied in total bacterial extracts from cells expressing these enzymes as GST fusion proteins. Neither Mch2 alpha nor Mch2 beta was able to cleave the YVAD substrate. Mch2 alpha, but not Mch2 beta, cleaved the DEVD substrate, but was 150-fold less active than CPP32.
CC	
CC	Sequence 4 AA;
SQ	

KW 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.
XX OS Synthetic.
XX CS
FH Key Modified-site Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 4 /note= "Optional attachment to aldehydes or ketones"
FT XX WO9820024-A1.
PN PD 14-MAY-1998.
XX 03-NOV-1997; 97WO-CA000824.
PR 04-NOV-1996; 96US-0030411P.
PA (MERI) MERCK FROSST CANADA INC.
PI Desmarais S, Friesen R, Zamponi R;
XX DR 1998-348101/30.
XX Peptide(s) useful in binding assays for tyrosine phosphatases or cysteine proteases - contain two or more 4-Phosphono(difluoromethyl) phenylalanine groups to improve binding affinity.
XX Example; Page 29; 59pp; English.
XX Variants of the apopain (caspase-3) peptide substrate can be used as ligands for the binding assay used in the invention. The invention provides a method for use in a scintillation proximity binding assay (SPA) for proteases and phosphatases. The method involves using mutated proteases and phosphatases whereby the catalytic cysteine residue of the enzymes are replaced with a serine or alanine residue to correct the problem of interference in SPA from extraneous oxidising and alkylating agents. The mutation affects the catalytic properties of the enzyme but does not affect their binding properties. The invention claims for new ligands for use in SPA which have increased binding affinity for a tyrosine phosphatase or cysteine protease. The ligands contain at least two 4-phosphono(difluoromethyl) phenylalanine groups which increase binding affinity of the ligand to its respective enzyme. The assay can be used to determine the ability of new ligands and compound mixtures to competitively bind with an enzyme. The method is claimed to allow a better usage of SPA in the discovery of compounds for the treatment and study of diseases, e.g. diabetes, cancer and osteoporosis.
XX Sequence 4 AA;
XX Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS Synthetic.
Qy 1 DEVD 4
Db 1 DEVD 4
RESULT 5 AAN56305
ID AAN56305 standard; peptide; 4 AA.
XX AC
XX DT 22-JUL-1998 (first entry)
XX Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.
XX KW N-acetyl-DEVD-methyl coumarinamide; MCA;
KW interleukin-1- beta-converting enzyme-like activity; ICE activity;
KW cysteine protease; investigation; substrate specificity.
XX

OS Synthetic.
XX PN JP10099075-A.
XX PR 30-SEP-1996; 96JP-00276813.
XX PA (SHIS) SHISEIDO CO LTD.
XX DR WPI; 1998-289868/26.
XX PT Protein with interleukin-1-beta converting enzyme-like activity - useful in investigation of substrate specificity in, e.g. Parkinson's disease.
XX Disclosure; Page 2; 5pp; Japanese.
XX The present sequence, N-acetyl-DEVD-methyl coumarinamide (MCA), CC represents a sequence that is cleaved by a protein with interleukin-1- beta converting enzyme (ICE)-like activity. The protein, which is obtained from human keratinocytes, has a relative molecular weight of 80 kDa. The ICE protein is part of the cysteine protease family and is useful for investigation of the mechanism of substrate specificity (e.g., Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma, cancer and apoptosis).
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 1 DEVD 4
RESULT 6 AAW48948
ID AAW48948 standard; protein; 4 AA.
Qy 1 DEVD 4
Db 1 DEVD 4
XX Apopain (caspase-3) peptide substrate.
XX DE Apopain (caspase-3) peptide substrate.
XX KW Apopain; caspase-3; protease; SPA; tyrosine phosphatase;
KW scintillation proximity binding assay; diabetes; cancer;
KW 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.
XX DT 26-OCT-1995 (first entry)
XX DE Apopain (caspase-3) peptide substrate.
XX KW Key
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 4
FT /note= "Optional attachment to aldehydes or ketones"
XX PN WO9820156-A1.
XX PD 14-MAY-1999.
XX PP 03-NOV-1997; 97WO-CA000825.
XX PR 04-NOV-1996; 96US-0030408P.
XX PA (MERI) MERCK FROSST CANADA INC.
XX PI Desmarais S, Friesen R, Gresser M, Kennedy B, Nicholson D,
PI Ramachandran C, Skorey K, Ford-Hutchinson A,
XX

XX DR WPI; 1998-348103/30.
 XX PT Enzyme binding assay for detection of useful compounds - uses mutant form
 PT of wild-type enzyme, in which serine replaces cysteine at active site, to
 PT reduce interference from oxidising/alkylating agents.
 XX Example; Page 28; 63pp; English.

XX Variants of the apopain (caspase-3) peptide substrate can be used as
 CC ligands for the binding assay used in the invention. The invention claims
 CC for a method for use in a scintillation proximity binding assay (SPA) for
 CC proteases and phosphatases. The method involves using mutated proteases
 CC and phosphatases whereby the catalytic cysteine residue of the enzymes
 CC are replaced with a serine or alanine residue to correct the problem of
 CC interference in SPA from extraneous oxidising and alkylating agents. The
 CC mutation affects the catalytic properties of the enzyme but does not
 CC affect their binding properties. The invention provides new ligands for
 CC use in SPA which have increased binding affinity for a tyrosine
 CC phosphatase or cysteine protease. The ligands contain at least two 4-
 CC phosphono(difluoromethyl) phenylalanine groups which increase binding
 CC affinity of the ligand to its respective enzyme. The assay can be used to
 CC determine the ability of new ligands and compound mixtures to
 CC competitively bind with an enzyme. The method is claimed to allow a
 CC better usage of SPA in the discovery of compounds for the treatment and
 CC study of diseases, e.g. diabetes, cancer and osteoporosis

XX Sequence 4 AA;
 Query Match Similarity 100.0%; Score 21; DB 2; Length 4;
 Matches 4; Conservative 0; Pred. No. 1.4e+06;
 Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

XX Sequence 4 AA;
 Query Match Similarity 100.0%; Score 21; DB 2; Length 4;
 Matches 4; Conservative 0; Pred. No. 1.4e+06;
 Mismatches 0; Indels 0; Gaps 0;

AC AAY15622;

XX AAY15622 standard; Peptide; 4 AA.
 AC AAY15622;
 XX DT 27-JUL-1999 (first entry)

XX Peptide used to make fluorescent reporter molecules.
 XX Fluorogenic fluorescent reporter molecule; enzyme substrate; apoptosis;
 KW protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent;
 KW cell death; viral protease activity.
 XX Synthetic.
 OS PN WO9918856-A1.
 XX PD 22-APR-1999.
 XX PF 09-OCT-1998; 98WO-US021231.
 XX PR 10-OCT-1997; 97US-0061582P.
 PR 03-MAR-1998; 98US-00033661.
 XX PA (CYTO-) CYTOVIA INC.

XX PI Weber E, Cai SX, Keana JFW, Drewe JA, Zhang H;
 XX DR 1999-312448/26.
 PT New fluorogenic or fluorescent reporter molecules.
 XX Claim 3; Page 160; 202pp; English.

XX AAY15618-Y15759 represent peptides used to make the fluorogenic or
 CC fluorescent reporter molecules of the invention. These molecules contain
 CC a peptide moiety (e.g. present sequence) which acts as a substrate for
 CC enzymes involved in apoptosis or protease or peptidase enzymes. The
 CC compounds can be used as fluorogenic or fluorescent substrates for
 CC enzymes. Depending on the peptide moiety used, the fluorescent molecules
 CC can be used for detecting or measuring the activity of an enzyme involved
 CC in the apoptosis cascade in cells; to determine whether a test compound
 CC has an effect on an enzyme involved in the apoptosis cascade in cells;
 CC for determining the sensitivity of an animal with cancer to treatment
 CC with chemotherapeutic agents or determining whether a test substance
 CC inhibits, prevents, causes or enhances cell death of test cells; for
 detecting or measuring the activity of a viral protease in cells; for
 determining whether a test compound has an effect on the activity of a
 CC viral protease in cells; and for measuring the activity or determining
 CC whether a test substance has an effect on the activity of a protease or
 CC peptidase in cells

XX SQ Sequence 4 AA;

Query Match Similarity 100.0%; Score 21; DB 2; Length 4;
 Matches 4; Conservative 0; Pred. No. 1.4e+06;
 Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 8
 AAY04114
 ID AAY04114 standard; peptide; 4 AA.

AC AAY04114;
 XX DT 15-JUN-1999 (first entry)

DB Enzyme component #2 caspase recognition sequence.

XX Cross-linked polypeptide assay; cross-linked enzyme component; cleavage;
 KW HIV; protease cleavage site.
 XX Synthetic.

OS XX WO9905537-A1.

XX PN WO9905537-A1.
 PD 11-FEB-1999.
 XX PP 23-JUL-1998; 98WO-US015343.

XX PR 30-JUL-1997; 97US-0090766.

XX PA (BOEFL) BOHRINGER MANNHEIM CORP.

PA Powell MJ, Khanna P, Eisenbeis SJ, Lingenfelter D, Tietze LF;

PI Manning W;
 XX DR 1999-190002/16.

XX New cross-linked enzyme components - which have inhibited ability to
 PT complement with other enzyme components to form an active enzyme complex.
 XX Example 10; Page 34; 56pp; English.

XX The present invention describes a cross-linked enzyme component (A),
 CC which: (i) has an inserted enzyme recognition site (ERS) in a polypeptide
 CC of the component; and (ii) has at least one covalent intrachain cross-
 CC link between amino acid side chains of the polypeptide. The component
 CC forms an enzymatically active complex with the polypeptide upon
 CC cleavage of the ERS, but is inhibited from forming this complex
 CC prior to cleavage. The complex has enzymatic activity which is different
 CC from that of beta-galactosidase. The component may be used for
 CC measurement of substances in biological samples. It is especially useful

CC for measurement of enzymes (e.g. proteases, particularly viral, phosphatase, glycosidase, amidase and esterase) in clinical samples, or CC for measurement of target polynucleotides. Assay methods using the new components exhibit extremely low inherent background signals due to reduction or inhibition of complementation of enzyme components prior to cleavage. The present sequence represents a peptide from an example of the present invention

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

RESULT 9
AAW68554 standard; protein; 4 AA.
ID AAW68554;
XX AC AAW68554;
XX DT 25-JAN-1995 (first entry)
DE Apopain aldehyde-inhibitor peptide L-761191.
XX Inhibitor; apopain; binding site; crystal structure; primer; PCR; amplification; Escherichia coli; apoptosis.
XX KW Synthetic.
OS PN JP11180B91-A.
XX PH PF Modified-site 1 Location/Qualifiers
PT /note= "acylated N-terminus"
PT Modified-site 4 /note= "contains C-terminal aldehyde group replacing carboxyl group"
PT
XX PN US5634228-A.
XX PD 10-NOV-1998.
XX PF 13-FEB-1997; 97US-00800007.
XX PR 13-FEB-1997; 97US-00800007.
XX PA (MERCK & CO INC.
PA (MERCK FROSST CANADA INC.
PI Thornberry NA, Gallant M, Pazil KM, Nicholson DW, Peterson EP, Rasper DM, Labelle M, Vaillancourt JP, Rotonda J, Ruei R, Becker JW, Gareau Y; Col 29; 22pp; English.

Claim 1; Col 1999-008706/01.

Identifying inhibitors of apopain by rational drug design - from ability to bind to the enzyme's substrate binding domain, potentially useful for inhibiting apoptosis, e.g. in treatment of acquired immune deficiency syndrome, autoimmune disease, infections etc.

XX The invention relates to the identification of inhibitors of apopain by designing and synthesising a potential inhibitor that will form non-covalent bonds with amino acids in the apopain substrate binding site, based upon the crystal structure co-ordinates of an apopain:acetyl-DEVD-CMO complex, testing it for apopain inhibition. Production of apopain for the binding studies comprises expression of the p17 and p12 subunits separately. This sequence represents an aldehyde-inhibitor of apopain designated L-761191. The apopain inhibitors are potentially useful for

CC inhibiting apoptosis
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

RESULT 10
AAV24411
ID AAY24411 standard; peptide; 4 AA.
XX AC AAY24411;
XX DT 20-SEP-1999 (first entry)
DE Caspase processing site peptide #2 in aldehyde form.
XX Human; caspase; anti-apoptosis; processing site; aldehyde; apoptosis; hepatitis; ischaemic cerebral disease; Alzheimer's disease; cancer; diarrhoea; bone marrow toxicity.
XX CS Homo sapiens.
OS Synthetic.
XX PN JP11180B91-A.
XX PD 06-JUL-1999.
XX PF 25-DEC-1997; 97JP-00356757.
XX PR 25-DEC-1997; 97JP-00356757.
XX PA (DAUC) DAIICHI PHARM CO LTD.
XX WPI; 1999-439401/37.
XX New anti-apoptosis agents - useful for treating hepatitis, ischemic cerebral diseases and Alzheimer's disease.
XX Claim 6; Page 6; 7pp; Japanese.

The present invention describes anti-apoptosis agent(s) containing human caspase and/or inhibitor(s) of its inducer(s), (especially human caspase-1, human caspase-3 and/or a human caspase-3 inducer), comprising de-processing the process of human caspase inhibitor into active type of human caspase inducer. Also describes are anti-apoptosis agent(s) containing modified protein comprising amino acid sequence around the processing site of caspase, especially aldehyde form of protein composed of amino acids of Tyr-Val-Ala-Asp, Asp-Glu-Val-Asp, and Glu-Ser-Met-Asp, especially Glu-Ser-Met-Asp, used for treatment of disease caused by apoptosis including hepatitis, ischaemic cerebral diseases, Alzheimer's disease, adverse reactions of bone marrow toxicity and diarrhoea due to administration of anticancer agent, especially hepatitis. The agents(s) are useful for treating disease caused by apoptosis e.g. ischaemic cerebral diseases, Alzheimer's disease, adverse reactions of bone marrow toxicity and diarrhoea due to administration of anticancer agent, especially hepatitis.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 1 DEVD 4

Db	1 DEV D 4	
RESULT 13		
AAV78347		
ID AAV78347	standard; peptide; 4 AA.	
AC		
XX		
DT 05-MAY-2000	(first entry)	
DE Caspase 1 peptide Dns-SS-DEVD-CHO.		
XX	Caspase; protein array; screening; biomolecular activity; proteomic;	
KW drug development; biosensor; diagnosis.		
XX	Unidentified.	
OS		
XX		
Key	Location/Qualifiers	
DE Modified-site 1	/note= "Asp is N-terminally modified to danyl-SS-Asp"	
FT Modified-site 4	/note= "Asp is C-terminally modified to Asp-CHO"	
XX		
PN WO200004332-A1.		
XX		
PD 27-JAN-2000.		
XX		
PF 14-JUL-1999;	99WO-US015971.	
XX		
PR 14-JUL-1998;	98US-00115455.	
XX		
PA (ZYOMX INC.		
XX		
PI Wagner P, Ault-Riche D, Nock S, Itin C;		
XX		
DR PT 2000-171289/15.		
XX		
PS Example 7; Page 55; 81pp; English.		
XX		
New arrays for analyzing components of a fluid sample, useful for drug development, functional proteomics, clinical diagnostics and biosensor.		
XX		
XX		
CC The present invention describes an array (I) of proteins comprising a substrate, at least one organic thinfilm on some or all of the substrate surface, and patches arranged in discrete, known regions on portions of the substrate surface covered by organic thinfilm. Each of the patches comprises a protein immobilised on the underlying organic thinfilm. The arrays can be used for screening proteins for their ability to interact with a component of a sample. They can also be used for assaying for protein-protein binding interactions or analytes. They can be used for drug development, proteomics, clinical diagnostics and biosensors. The present sequence represents a peptide used in the exemplification of the present invention.		
CC Sequence 4 AA;		
CC Query Match 100.0%; Score 21; DB 3; Length 4;		
CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;		
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
CC SQ Sequence 4 AA;		
CC Query Match 100.0%; Score 21; DB 3; Length 4;		
CC Best Local Similarity 100.0%; Pred. No. 1.4e-06;		
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
CC Qy 1 DEV D 4		
CC Db 1 DEV D 4		
RESULT 14		
AAV69646		
ID AAV69646	standard; peptide; 4 AA.	
XX		
AC AAV69646;		
XX		
DT 08-MAY-2000 (first entry)		

ID AAY99958 standard; peptide; 4 AA.
 XX
 AC AAY99958;
 XX
 DT 27-OCT-2000 (first entry)
 XX
 DE Tetrapeptide aldehyde which is a potent inhibitor of caspase-3.
 KW Inhibitor; apoptosis; cardiac; cerebral ischemia; stroke;
 KW type I diabetes; immune deficiency syndrome; HIV; AIDS; cerebral;
 KW spinal chord trauma; injury; alopecia; ageing; Parkinson's disease;
 KW Alzheimer's disease; Down's syndrome; spinal muscular atrophy;
 KW multiple sclerosis; neurodegenerative disorders; caspase;
 KW gamma-ketoacid tetrapeptide; cysteine proteases.
 XX
 OS Unidentified.
 XX
 Key Location/Qualifiers
 FT Modified-site 1
 /note= "N-terminal acetyl"
 FT Modified-site 4
 /note= "D(CHO)"
 XX
 PN WO20032620-A1.
 XX
 PD 08-JUN-2000.
 XX
 PP 30-NOV-1999 ; 99WO-CA001145.
 XX
 PR 02-DEC-1998 ; 98US-0110567P.
 XX
 PA (MERCK) MERCK FROSST CANADA & CO.
 PI Grimm EL, Renaud J, Aspiotis R, Bayly CI, Zamboni R, Black S;
 XX
 DR 2000-4-12282/35.
 XX
 PT New gamma-ketoacid tetrapeptide compounds having caspase-3 inhibiting
 PT activity, useful for treating e.g. Parkinson's disease, organ damage
 PT during transportation, alopecia and ageing.
 XX
 Disclosure: Page 4; 121pp; English.
 XX
 CC The present invention relates to gamma-ketoacid tetrapeptide compounds,
 CC which have been found to inhibit caspase-3. Inhibition of caspase
 CC activity is known to inhibit apoptosis. The present sequence is a
 CC tetrapeptide aldehyde which is a very potent inhibitor of caspase-3. This
 CC peptide was designed to mimic the caspase-3 recognition site (see
 CC AA99957). Caspase-3 inhibitors may be used for treating cardiac and
 CC cerebral ischemia reperfusion injury (e.g. stroke), type I diabetes,
 CC immune deficiency syndrome (e.g. HIV or AIDS), cerebral and spinal chord
 CC trauma injury, alopecia, ageing, Parkinson's disease, Alzheimer's
 CC disease, Down's syndrome, spinal muscular atrophy, multiple sclerosis and
 CC neurodegenerative disorders. They may also be used for treating other
 CC caspase-3 mediated diseases.
 XX
 SQ Sequence 4 AA:
 Query Match Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Prcd. No. 1.4e-06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEV D
 |||||
 Db 1 DEV D
 |||||

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OM Protein - protein search, using SW model

Run on: May 24, 2004, 14:36:17 ; Search time 16.5 Seconds

(without alignments)
12.515 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgm2_6/ptodata/2/iaa/5A/COMB.pep:*
- 2: /cgm2_6/ptodata/2/iaa/5B/COMB.pep:*
- 3: /cgm2_6/ptodata/2/iaa/6A/COMB.pep:*
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- 5: /cgm2_6/ptodata/2/iaa/PCFUS/COMB.pep:*
- 6: /cgm2_6/ptodata/2/iaa/backfiled1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	4	1	US-08-446-925-9	Sequence 9, Appli
2	21	100.0	4	2	US-08-800-00A-10	Sequence 10, Appli
3	21	100.0	4	2	US-09-146-921-9	Sequence 9, Appli
4	21	100.0	4	2	US-08-915-414A-1	Sequence 1, Appli
5	21	100.0	4	2	US-08-896-855-9	Sequence 9, Appli
6	21	100.0	4	2	US-08-712-858-2	Sequence 2, Appli
7	21	100.0	4	3	US-08-926-588-39	Sequence 39, Appli
8	21	100.0	4	3	US-08-802-981-2	Sequence 2, Appli
9	21	100.0	4	3	US-09-210-731-42	Sequence 2, Appli
10	21	100.0	4	3	US-09-167-921-42	Sequence 42, Appli
11	21	100.0	4	3	US-09-210-736-1	Sequence 1, Appli
12	21	100.0	4	3	US-08-761-483-3	Sequence 3, Appli
13	21	100.0	4	3	US-08-761-483-10	Sequence 10, Appli
14	21	100.0	4	3	US-09-123-733-42	Sequence 42, Appli
15	21	100.0	4	3	US-09-058-961-2	Sequence 2, Appli
16	21	100.0	4	3	US-09-130-193-1	Sequence 1, Appli
17	21	100.0	4	3	US-09-130-193-7	Sequence 7, Appli
18	21	100.0	4	3	US-09-130-193-12	Sequence 12, Appli
19	21	100.0	4	3	US-09-130-193-15	Sequence 15, Appli
20	21	100.0	4	3	US-09-317-952-5	Sequence 5, Appli
21	21	100.0	4	3	US-09-309-005-1	Sequence 1, Appli
22	21	100.0	4	3	US-08-869	Sequence 1, Appli
23	21	100.0	4	3	US-09-257-218-81	Sequence 81, Appli
24	21	100.0	4	3	US-09-257-218-82	Sequence 82, Appli
25	21	100.0	4	3	US-09-311-750-81	Sequence 81, Appli
26	21	100.0	4	3	US-09-311-750-82	Sequence 82, Appli
27	21	100.0	4	3	US-09-291-692-71	Sequence 71, Appli

RESULT 1
US-08-446-925-9
Sequence 9, Application US/08446925
Patent No. 5672500
GENERAL INFORMATION:
APPLICANT: Litwack, Gerald S.
ALINEMRI, Enad S.
APPLICANT: Fernandez-Alnemri, Teresa Mch2, AN APOPTOTIC CYSTEINE PROTEASE
TITLE OF INVENTION: PROTEASE, AND COMPOSITIONS FOR MAKING AND METHODS OF USING THE SAME
TITLE OF INVENTION: NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Woodcock, Walsburn, Kurtz, Mackiewicz &
ADDRESSSEE: No. 5672500
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446, 925
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REDOCKET NUMBER: TJJ-1508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 9;
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-046-125-9
Query Match Score 21/ DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Sequence 10, Application US/08800007A-10

PATENT NO. 5834228

GENERAL INFORMATION:

APPLICANT: Becker, Joseph Donald
Rotonda, Jennifer
Thornberry, Nancy
Fazil, Kimberly
Gallant, Michel
Gareau, Yves
Labeille, Marc

APPLICANT: Peterson, Erin
Reaper, Dita

TITLE OF INVENTION: CRYSTAL STRUCTURE OF APOPAIN

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: COPPOLA - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FasterEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,007A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 19644
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEX: 732-534-4720

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Prd. No. 3e05; Mismatches 0; Indels 0; Caps 0;

RESULT 3

Sequence 9, Application US/09146331

PATENT NO. 5958720

GENERAL INFORMATION:

APPLICANT: Litwack, Gerald
Alnemri, Bimal S.

APPLICANT: Fernandez-Alnemri, Teresa
Title of Invention: Nch2, AN APOPTOTIC CYSTEINE PROTEASE, AND COMPOSITIONS FOR MAKING AND METHODS OF USING THE SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Associates
No. 5958720r15

STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/146,331
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/896,885
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUJ-1508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-4349
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-146-331-9

Query Match Score 100.0%; DB 2; Length 4;
Best Local Similarity 100.0%; Prd. No. 3e05; Mismatches 0; Indels 0;

Qy 1 DEV D 4
Db 1 DEV D 4

RESULT 4

US-08-915-414A-1

Sequence 1, Application US/08915414A
Patent No. 5976822

GENERAL INFORMATION:

APPLICANT: LANDRUM, ET AL.
PATENT NO. 5976822

TITLE OF INVENTION: METHOD AND REAGENT FOR MONITORING APOPTOSIS AND DISTINGUISHING APOPTOSIS FROM NECROSIS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: MITCHELL ALTER, COULTER INTERN. CORP.
STREET: 11180 SW 147 AVE.
CITY: MIAMI
STATE: FLORIDA
COUNTRY: USA
ZIP: 33196

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 6.0/95

CURRENT APPLICATION DATA:

RESULT 5

Sequence 9, Application US/09146331

PATENT NO. 5958720

GENERAL INFORMATION:

APPLICANT: Landrum, et al.
Title of Invention: Method and Reagent for Monitoring Apoptosis and Distinguishing Apoptosis from Necrosis

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: MITCHELL ALTER, COULTER INTERN. CORP.
STREET: 11180 SW 147 AVE.
CITY: MIAMI
STATE: FLORIDA
COUNTRY: USA
ZIP: 33196

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 6.0/95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/915,414A
 FILING DATE: 20-AUG-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/444,051
 FILING DATE: 18-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MITCHELL B. ALTER
 REGISTRATION NUMBER: 28,684
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (305) 380-3636
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid acids
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: Peptide

US-08-915-114A-1

Query Match Similarity 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. NC 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV'D 4
 Db 1 DEV'D 4

RESULT 5
 US-08-896-885-9

Sequence 9 Application US/08896685
 Patent No. 5985640

GENERAL INFORMATION:
 APPLICANT: Litwack, Gerald
 ALINEMRI, Emad S.
 APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE PROTEASE AND COMPOSITIONS FOR MAKING AND METHODS OF USING THE SAME

TITLE OF INVENTION: METHODS OF USING THE SAME

TITLE OF INVENTION: METHODS OF USING THE SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
 ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz &
 ADDRESS: No. 598564018
 STREET: One Liberty Place, 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/896,885
 FILING DATE: 18-JUL-1997
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/446,925
 FILING DATE: 18-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TTU-1508

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids

TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-896-885-9

Query Match Similarity 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. NC 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV'D 4
 Db 1 DEV'D 4

RESULT 6
 US-08-712-878-2

Sequence 2 Application US/08712878
 Patent No. 598563

GENERAL INFORMATION:
 APPLICANT: Su, Michael
 APPLICANT: Gu, Yong
 APPLICANT: Livingston, David J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DECREASING IGF1 AND IFN-GAMMA PRODUCTION BY ADMINISTERING AN ICE INHIBITOR

TITLE OF INVENTION: INHIBITOR

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr.
 STREET: 1551 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/712,878
 FILING DATE: 12-SEP-1996
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: VP1/96-05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-296-3000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "aspartic acid is acetylated"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /note= "aspartic acid carboxy terminal is reduced to an aldehyde"

Query Match Similarity 100.0%; Score 21; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. NC 3e+05; Mismatches 0; Indels 0; Gaps 0;

US-08-712-878-2

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 7
 US-09-226-568-39
 ; Sequence 39, Application US/09226568
 ; GENERAL INFORMATION:
 ; APPLICANT: Achermann, Elizabeth J.
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Marcussen, Eric G.
 ; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
 ; TITLE OF INVENTION: bcl-2-Related Proteins
 ; FILE REFERENCE: ISPH-0337
 ; CURRENT APPLICATION NUMBER: US/09/226,568
 ; CURRENT FILING DATE: 1999-01-07
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 39
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09-226-568-39

Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 8
 US-08-802-981-2
 ; Sequence 2, Application US/08802981
 ; Patent No. 6037137
 ; GENERAL INFORMATION:
 ; APPLICANT: Komoriya, Akira
 ; APPLICANT: Packerd, Beverly S.
 ; TITLE OF INVENTION: Compositions for the Detection of Enzyme
 ; NUMBER OF SEQUENCES: 231
 ; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/802,981
 FILING DATE: 20-FEB-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE DOCKET NUMBER: 016865-000300US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-802-981-2

RESULT 9
 US-09-270-735-2
 ; Sequence 2, Application US/09270735
 ; Patent No. 6153591
 ; GENERAL INFORMATION:
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Drew, John
 ; APPLICANT: Wang, Yan
 ; APPLICANT: Weber, Eckhard
 ; TITLE OF INVENTION: Dipeptide Caspase Inhibitors and the Use Thereof
 ; FILE REFERENCE: 1735_0010001
 ; CURRENT APPLICATION NUMBER: US/09/270,735
 ; CURRENT FILING DATE: 1999-03-16
 ; EARLIER APPLICATION NUMBER: 60/078,051
 ; EARLIER FILING DATE: 1998-03-16
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09-270-735-2

Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 10
 US-09-167-921-42
 ; Sequence 42, Application US/09167921A
 ; Patent No. 6172216
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Monia, Brett P.
 ; APPLICANT: Nickoloff, Brian J.
 ; APPLICANT: Zhang, QingQing
 ; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
 ; FILE REFERENCE: ISPH-0324
 ; CURRENT APPLICATION NUMBER: US/09/167,921A
 ; CURRENT FILING DATE: 1998-10-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 42
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: caspase assay substrate

US-09-167-921-42

Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

FEATURE: Peptide

OTHER INFORMATION: Peptide

Query Match 100.0%; Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

OTHER INFORMATION: Peptide

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/761,483

FILING DATE: 06-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James P.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: VPI/96-01CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000

TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE: Modified-site

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "Aspartic acid is

OTHER INFORMATION: acetylated"

US-08-761-483-3

Query Match

Score 21;

DB 3;

Length 4;

Best Local Similarity

100.0%;

Pred. No.

3e+05;

Indels

0;

Gaps

0;

Gaps

C;

Matches

4;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Gaps

C;

Qy

1 DEVD 4

Db

1 DEVD 4

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/761,483
 FILING DATE: 06-DEC-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 10:
 LENGTH: 4 amino acids
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /note= "aspartic acid is derivatized with amino-4-methylcoumarin"
 US-08-761-483-10

Query Match Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV D 4
 Db 1 DEV D 4

RESULT 14
 Sequence 42, Application US/09323743
 / Patent No. 614386
 GENERAL INFORMATION:
 / APPLICANT: Bennett, C. Frank
 / APPLICANT: Monia, Brett P.
 / APPLICANT: Dean, Nicholas M.
 / APPLICANT: Nicholoff, Brian J.
 / APPLICANT: Zhang, QingQing
 TITLE OF INVENTION: Antilense Modulation of bcl-x Expression
 FILE REFERENCE: ISPH-0368
 CURRENT APPLICATION NUMBER: US/09/323,743
 CURRENT FILING DATE: 1999-06-01
 EARLIER APPLICATION NUMBER: 09/277,020
 EARLIER FILING DATE: 1998-03-26
 EARLIER APPLICATION NUMBER: 09/157,921
 EARLIER FILING DATE: 1998-10-07
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 42
 LENGTH: 4

Query Match Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV D 4
 Db 1 DEV D 4

RESULT 15
 Sequence 2, Application US/09058969A
 / Patent No. 6228603
 GENERAL INFORMATION:
 / APPLICANT: Reed, John C.
 / APPLICANT: Devereaux, Quinn
 / APPLICANT: Salvesen, Guy S.
 / APPLICANT: Takahashi, Ryosuke
 / APPLICANT: Roy, Natalie
 TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of Caspase Activity
 FILE REFERENCE: LJ 3080
 CURRENT APPLICATION NUMBER: US/09/058,969A
 CURRENT FILING DATE: 1998-04-10
 EARLIER APPLICATION NUMBER: 08/862,087
 EARLIER FILING DATE: 1997-05-22
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 4

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence

US-09-058-969-2
 Query Match Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEV D 4
 Db 1 DEV D 4

Search completed: May 24, 2004, 14:39:00

Job time : 17.5 secs

Query Match Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-323-743-42
 Query Match Score 21; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.⁶
 Copyright (c) 1993 - 2004 Compugen Ltd.

CM Protein - Protein search, using SW model

Run on: May 24, 2004, 14:39:37 ; Search time 38 Seconds
 (without alignments)
 29,360 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

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 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
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Database : Published Applications AA:^{*}

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	9 US-09-045-620-4	Sequence 4, Appli
2	21	100.0	4	9 US-09-734-846-42	Sequence 42, Appli
3	21	100.0	4	9 US-09-799-463-2	Sequence 2, Appli
4	21	100.0	4	9 US-09-735-362A-85	Sequence 85, Appli
5	21	100.0	4	9 US-09-799-993-2	Sequence 2, Appli
6	21	100.0	4	9 US-09-952-768-71	Sequence 71, Appli
7	21	100.0	4	9 US-09-856-754-111	Sequence 11, Appli
8	21	100.0	4	9 US-09-987-417-3	Sequence 3, Appli
9	21	100.0	4	9 US-09-737-255-1	Sequence 1, Appli
10	21	100.0	4	9 US-09-920-332-1	Sequence 8, Appli
11	21	100.0	4	9 US-09-845-028-8	Sequence 52, Appli
12	21	100.0	4	9 US-09-954-697-52	Sequence 5, Appli
13	21	100.0	4	9 US-09-947-387-5	Sequence 2, Appli
14	21	100.0	4	10 US-09-161-112-2	Sequence 7, Appli
15	21	100.0	4	10 US-09-866-512A-7	Sequence 6, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1 SEQ ID NO: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: caspase-specific peptide

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (4)

OTHER INFORMATION: aminomethyl coumarin linked with residue 4
 US-09-045-620-4

Query Match Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Mismatches 0; Indels 0; Gaps 0;

OY

1 DEVD 4

Db 1 DEVD 4

RESULT 2
 US-09-734-846-42

Sequence 42, Application US/09734846
 GENERAL INFORMATION:
 APPLICANT: Bennett, C. Frank
 APPLICANT: Dean, Nicholas M.
 APPLICANT: Monia, Brett P.
 APPLICANT: Nickoloff, Brian J.
 APPLICANT: Zhang, QirGong
 TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
 CURRENT APPLICATION NUMBER: US/09/734,846
 CURRENT FILING DATE: 2000-12-12
 PRIOR APPLICATION NUMBER: 09/277,020
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 09/167,921
 PRIOR FILING DATE: 1998-10-07
 PRIOR APPLICATION NUMBER: 09/322,743
 PRIOR FILING DATE: 1999-06-02
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 42
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense Oligonucleotide
 US-09-734-846-42

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 4
 US-09-735-363A-85
 Sequence 85, Application US/09735363A
 GENERAL INFORMATION:
 APPLICANT: Filion, Mario
 APPLICANT: Phillip, Nigel
 TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
 CURRENT APPLICATION NUMBER: US/09/735,363A
 CURRENT FILING DATE: 2000-12-12
 PRIOR APPLICATION NUMBER: 60/170,325
 PRIOR FILING DATE: 1999-12-13
 PRIOR APPLICATION NUMBER: 60/228,925
 PRIOR FILING DATE: 2000-08-29
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn Version 3.0
 SEQ ID NO: 85
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Peptide
 US-09-735-363A-85

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 5
 US-09-799-994-2
 Sequence 2, Application US/09799994
 GENERAL INFORMATION:
 APPLICANT: Reed, John C.
 APPLICANT: Deveraux, Quinn
 APPLICANT: Salvesen, Guy S.
 APPLICANT: Takahashi, Ryosuke
 APPLICANT: Roy, Natalie
 TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of Apoptosis (IAP) Protein Regulation of Caspase Activity
 FILE REFERENCE: LJ 3080
 CURRENT APPLICATION NUMBER: US/09/599,994
 CURRENT FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: 09/058,969
 PRIOR FILING DATE: 1998-04-10
 PRIOR APPLICATION NUMBER: 08/862,087
 PRIOR FILING DATE: 1997-05-22
 NUMBER OF SEQ ID NOS: 12
 SEQ ID NO: 2
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence
 US-09-799-994-2

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 6

Sequence 43, Application US/09799946
 GENERAL INFORMATION:
 APPLICANT: Salvesen, Guy S.
 APPLICANT: Deveraux, Quinn
 APPLICANT: Takahashi, Ryosuke
 APPLICANT: Roy, Natalie
 TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of Apoptosis (IAP) Protein Regulation of Caspase Activity
 FILE REFERENCE: LJ 3080
 CURRENT APPLICATION NUMBER: US/09/799,463
 CURRENT FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: 09/058,969
 PRIOR FILING DATE: 1998-04-10
 PRIOR APPLICATION NUMBER: 08/862,087
 PRIOR FILING DATE: 1997-05-22
 NUMBER OF SEQ ID NOS: 12
 SEQ ID NO: 2
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence
 US-09-799-994-3

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

US-09-952-768-71
Sequence 71, Application US/09952768
Patent No. US20020035242A1

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa

Litwack, Gerald
Armstrong, Robert
Tomaselli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE, NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEES: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,768

FILING DATE: 10-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 480140.424C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-0331

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 71:

US-09-952-768-71

Query Match

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Best Local Similarity 100.0%; Pred. No. 1e+06;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

RESULT 7

US-09-858-754-11

Sequence 11, Application US/09858754

Patent No. US20020055130A1

GENERAL INFORMATION:

APPLICANT: Johnson, Gary L.

TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS

FILE REFERENCE: CPI-042

CURRENT APPLICATION NUMBER: US/09/858,754

CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 09/021,130

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 60/039,740

PRIOR FILING DATE: 1997-02-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 4

TYPE: PRT

ORGANISM: synthetic construct

US-09-858-754-11

Query Match

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Best Local Similarity 100.0%; Pred. No. 1e+06;

Mismatches 0; Indels 0; Gaps 0;

US-09-858-754-11

Query Match

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Best Local Similarity 100.0%; Pred. No. 1e+06;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

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RESULT 8

US-09-987-417-3

Sequence 3, Application US/09987417

Patent No. US2002005863A1

GENERAL INFORMATION:

APPLICANT: Cai, Sui Xiong

APPLICANT: Weber, Rickard

APPLICANT: Wang, Yan

APPLICANT: Mills, Gordon B.

APPLICANT: Green, Douglas R.

TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof

FILE REFERENCE: 1735.0350003

CURRENT APPLICATION NUMBER: US/09/987,417

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 09/545,565

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: US 6/0/128,545

PRIOR FILING DATE: 1999-04-09

PRIOR APPLICATION NUMBER: US 6/0/158,370

PRIOR FILING DATE: 1999-10-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 4

TYPE: PRT

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: caspase 3 substrate

US-09-987-417-3

Query Match

100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

RESULT 9

US-09-737-255-1

Sequence 1, Application US/09737255

Patent No. US2002007441A1

GENERAL INFORMATION:

APPLICANT: Rehentulla, Alnawaz

APPLICANT: Ross, Brian D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING

PROTEOLYTIC ACTIVITY

FILE REFERENCE: 11203-003001

CURRENT APPLICATION NUMBER: US/09/737,255

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 4

TYPE: PRT

ORGANISM: Mus musculus

US-09-737-255-1

Query Match

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Best Local Similarity 100.0%; Pred. No. 1e+06;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

RESULT 10
 US-09-940-332-1
 ; Sequence 1, Application US/09920332
 ; Patent No. US2002007673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kshabhatla, Shailaja
 ; APPLICANT: Green, Douglas R.
 ; APPLICANT: Tseng, Ben
 ; TITLE OF INVENTION: Method of Identifying Immunostimulatory Agents
 ; FILE REFERENCE: 1735.0470001/RWEALS
 ; CURRENT APPLICATION NUMBER: US/09/920,332
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: US 60/222,897
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
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 ; NAME/KEY: MOD RES
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 ; OTHER INFORMATION: ACETYLATION
 ; US-09-940-332-1

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 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 13
 US-09-947-387-5
 ; Sequence 5, Application US/09947387
 ; Patent No. US20020150885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Edward
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drews, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735.0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: US 60/115,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US 09/168,688
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
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 ; LENGTH: 4
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 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-09-947-387-5

Query Match 100.0%; Score 21; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 14
 US-09-161-172-2
 ; Sequence 2, Application US/09161172
 ; Publication No. US20030044776A1

RESULT 12
 US-09-954-697-52

GENERAL INFORMATION:
 / APPLICANT: Dickens, James A.
 / APPLICANT: Miller, Scott W.
 / APPLICANT: Ghosh, Soumitra S.
 / APPLICANT: Davis, Robert E.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
 / AGENTS THAT ALTER MITOCHONDRIAL PERMEABILITY
 / TRANSITION PORES
 / TITLE OF INVENTION:
 / FILE REFERENCE: 660088,418
 / CURRENT APPLICATION NUMBER: US/09/161,172
 / CURRENT FILING DATE: 1998-09-25
 / NUMBER OF SEQ ID NOS: 2
 / SOFTWARE: Fast-SEQ for Windows Version 4.0
 / SEQ ID NO 2
 / LENGTH: 4
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: caspase-3 specific fluorogenic peptide substrate

US-09-161-172-2

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RESULT 15
 US-09-866-512A-7
 Sequence 7, Application US/09866512A
 Publication No US2003003954A1

GENERAL INFORMATION:
 / APPLICANT: Meade, Thomas J
 / TITLE OF INVENTION: Magnetic Resonance Imaging Agents for the Detection of Physiology
 / TITLE OF INVENTION: Agents
 / FILE REFERENCE: A-56634-7

CURRENT APPLICATION NUMBER: US/09/866,512A
 CURRENT FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: US 60/287,619
 PRIOR FILING DATE: 2001-05-26
 PRIOR APPLICATION NUMBER: US 08/460,511
 PRIOR FILING DATE: 1995-06-02
 PRIOR APPLICATION NUMBER: US 08/486,968
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: US 08/971,855
 PRIOR FILING DATE: 1997-11-17
 PRIOR APPLICATION NUMBER: US 09/134,072
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 09/866,512
 PRIOR FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: US 09/405,046
 PRIOR FILING DATE: 1999-09-27
 PRIOR APPLICATION NUMBER: US 60/063,328
 PRIOR FILING DATE: 1997-10-27
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 7
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 / OTHER INFORMATION: could be from any mammal.

US-09-866-512A-7

Query Match 100.0%; Score 21; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DEVD 4
Db	1 DEVD 4

MS-2
B6a

GenCore version 5.1.6
 Copyright (C) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: May 24, 2004, 14:38:22 ; Search time 175 Seconds

(without alignments)

22.310 Million cell updates/sec

Title: US-09-765-105A-2
 Perfect score: 21
 Sequence: 1 DBVD 4

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Searched: 6019581 seqs, 976053577 residues

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30: /cnr2_6_ptodata/2/paa/us104_comb.pep:*

31: /cnr2_6_ptodata/2/paa/us105_comb.pep:*

32: /cnr2_6_ptodata/2/paa/us107_comb.pep:*

33: /cnr2_6_ptodata/2/paa/us60_comb.pep:*

Pred. No. is the number of results predicted by chance to have a a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match Length	DB ID	Description
No.	%			

SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

RESULT 1
 PCT/US00-02329-1
 Application PC/US0002329
 GENERAL INFORMATION:
 APPLICANT: Cytovia, Inc.
 TITLE OF INVENTION: Methods of Identifying Potentially Therapeutically Effective Antineoplastic Agents with Viable Cultured Cells Having an Intact Cell Membrane and Product by

FILE REFERENCE: 1735.032PC02
 CURRENT APPLICATION NUMBER: PCT/US00-02329
 CURRENT FILING DATE: 2000-02-01
 EARLIER APPLICATION NUMBER: 60/118,102
 EARLIER FILING DATE: 1999-02-01
 EARLIER APPLICATION NUMBER: 09/454,595
 EARLIER FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NO: 9
 SOFTWARE: PatentIn Ver. 2.1

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
PCT-US00-02329-1

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 2

PCT-US00-02332-1
Sequence 1, Application PC/TUS0002332
GENERAL INFORMATION:
APPLICANT: CYTOVIA, INC.
APPLICANT: CAL, SUI XIONG
APPLICANT: ZHENG, HAN-ZHONG
APPLICANT: WANG, YAN
APPLICANT: TSING, BEN
APPLICANT: KASIBHATLA, SHAILAJA
APPLICANT: DREW, JOHN A.
TITLE OF INVENTION: GAMBOGIC ACID, ANALOGS AND DERIVATIVES AS ACTIVATORS OF FILE REFERENCE: CAPSESSES AND INDUCERS OF APOPTOSIS
CURRENT APPLICATION NUMBER: PCT/US00/02332
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
PCT-US00-02332-1

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 3

PCT-US00-09319-3
Sequence 3, Application PC/TUS0009319
GENERAL INFORMATION:
APPLICANT: Cytovia, Inc.
APPLICANT: Cai, Sui Xiong
APPLICANT: Weber, Eckard
APPLICANT: Wang, Yan
APPLICANT: Green, Douglas R.
APPLICANT: Mills, Goddon B.
TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof
FILE REFERENCE: 1735.03PC02
CURRENT APPLICATION NUMBER: PCT/US00/09319
CURRENT FILING DATE: 2000-04-07
EARLIER APPLICATION NUMBER: US 60/128,545
EARLIER FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 60/158,370
EARLIER FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown Organism

; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: caspase 3
; OTHER INFORMATION: Substrate
PCT-US00-09319-3

Query Match Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 4

PCT-US00-14451-42
Sequence 42, Application PC/TUS0014451
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickloff, Brian J.
APPLICANT: Zhang, QingQing
APPLICANT: ISIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPE-0460
CURRENT APPLICATION NUMBER: PCT/US00/14451
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/323,743
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/167,921
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 09/277,020
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
PCT-US00-14451-42

RESULT 5
PCT-US01-04137-1
Sequence 1, Application PC/TUS0104137
GENERAL INFORMATION:
APPLICANT: Fodor, William L.
APPLICANT: ALEXION PHARMACEUTICALS, INC.

TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND METHODS OF USE THEREOF
FILE REFERENCE: 1087-15PCT
CURRENT APPLICATION NUMBER: PCT/US01/04137
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Caspase
OTHER INFORMATION: Inhibitor

PCT-US01-04137-1
 Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 6
 PCT-US01-48256-1
 Sequence 1, Application PC/TUS0148256
 GENERAL INFORMATION:
 APPLICANT: Regents of the University of Michigan
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
 TITLE OF INVENTION: PROTEOLYTIC ACTIVITY
 FILE REFERENCE: 11:203-003W01
 CURRENT APPLICATION NUMBER: PCT/US01/48256
 CURRENT FILING DATE: 2001-12-13
 PRIOR APPLICATION NUMBER: 09/737,255
 PRIOR FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FASEREQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Mus musculus
 PCT-US01-48226-1

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 7
 PCT-US02-04060-52
 Sequence 52, Application PC/TUS0204060
 GENERAL INFORMATION:
 APPLICANT: Massachusetts Institute of Technology, et al.
 TITLE OF INVENTION: Peptides Inhibit Poly-Glutamine Aggregation
 FILE REFERENCE: M0656/7062WO (JRV)
 CURRENT APPLICATION NUMBER: PCT/US02/04060
 CURRENT FILING DATE: 2002-02-11
 PRIOR APPLICATION NUMBER: US 60/267,898
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/334,891
 PRIOR FILING DATE: 2001-11-15
 NUMBER OF SEQ ID NOS: 52
 SOFTWARE: FastaIn version 3.1
 SEQ ID NO 52
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Caspase Inhibitor
 PCT-US02-04060-52

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 8
 PCT-US2-15198-1
 Sequence 1, Application PC/TUS0215198
 GENERAL INFORMATION:
 APPLICANT: CYTOVIA, INC.
 APPLICANT: CAI, SUI XIONG

PCT-US02-07569-1
 Sequence 1, Application PC/TUS0207569
 GENERAL INFORMATION:
 APPLICANT: Cytovia, Inc.
 TITLE OF INVENTION: Multifluoro-substituted Chalcones and Analogs as Activators of Apoptosis and the Use Thereof
 FILE REFERENCE: 1735.054PC01
 CURRENT APPLICATION NUMBER: PCT/JS02/07569
 CURRENT FILING DATE: 2002-02-14
 PRIOR APPLICATION NUMBER: 60/275,473
 PRIOR FILING DATE: 2001-03-14
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fluorogenic Substrate
 PCT-US02-07569-1

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 9
 PCT-US02-14722-1
 Sequence 1, Application PC/TUSS0214722
 GENERAL INFORMATION:
 APPLICANT: Cytovia, Inc.
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Kasibhatla, Shailaja
 APPLICANT: Drew, John
 APPLICANT: Reddy, P. Sarjeeva
 APPLICANT: Zhang, Han-Zhong
 TITLE OF INVENTION: Substituted N'-(Arylcarbonyl)-Benzhydrazides, N'-(Arylcarbonyl)-Benzylidene-hydrazides And Analogs as Activators and Inducers of Apoptosis And The Use Thereof
 FILE REFERENCE: 1735.056PC01
 CURRENT APPLICATION NUMBER: PCT/US02/14722
 CURRENT FILING DATE: 2002-05-10
 PRIOR APPLICATION NUMBER: US 60/289,803
 PRIOR FILING DATE: 2001-05-10
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fluorogenic substrate
 PCT-US02-14722-1

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 10
 PCT-US2-15198-1
 Sequence 1, Application PC/TUS0215198
 GENERAL INFORMATION:
 APPLICANT: CYTOVIA, INC.
 APPLICANT: CAI, SUI XIONG

APPLICANT: XUO LIPEN
 APPLICANT: STORER, RICHARD
 APPLICANT: ATTARDO, GIORGIO
 TITLE OF INVENTION: 7-B-FUSED 4H-CHROMENE AND ANALOGS AS ACTIVATORS OF CASPASES AND
 TITLE OF INVENTION: OF APOPTOSIS AND THE USE THEREOF
 FILE REFERENCE: 1735.065PC01
 CURRENT FILING DATE: 2002-05-16
 PRIOR FILING DATE: 2001-05-16
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fluorogenic substrate
 PCT-US02-15398-1

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 11
 PCT-US02-15401-1
 Sequence 1, Application PC/TUS0215401
 GENERAL INFORMATION:
 APPLICANT: Cytovia, Inc.
 APPLICANT: Shire BioChem, Inc.
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Zhang, Hong
 APPLICANT: Kemitzer, William E.
 APPLICANT: Jiang, Songchun
 APPLICANT: Drewe, John A.
 APPLICANT: Storer, Richard
 TITLE OF INVENTION: Substituted Coumarins and Quinolines and Analogs as Activators of Caspases and the Use Thereof
 FILE REFERENCE: 1735.066PC01
 CURRENT FILING DATE: 2002-05-16
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fluorogenic substrate
 PCT-US02-15401-1

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 12
 PCT-US02-15713-1
 Sequence 1, Application PC/TUS0215713
 GENERAL INFORMATION:
 APPLICANT: FE CORPORATION (NY)
 APPLICANT: YAN, Xiongwei
 APPLICANT: MIRAGLIA, Sheri
 APPLICANT: YUAN, Pau M

TITLE OF INVENTION: PEPTIDE CONJUGATES AND FLUORESCENCE DETECTION METHODS FOR
 TITLE OF INVENTION: INTRACELLULAR CASPASE ASSAY
 FILE REFERENCE: 4568NO
 CURRENT APPLICATION NUMBER: PCT/US02/15713
 CURRENT FILING DATE: 2002-05-15
 PRIOR APPLICATION NUMBER: US 09/862,224
 PRIOR FILING DATE: 2001-02-21
 NUMBER OF SEQ ID NOS: 3
 SEQ ID NO: 1
 SOFTWARE: PatentIn version 3.1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US02-15713-1
 Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4
 RESULT 13
 PCT-US02-17108-1
 Sequence 1, Application PC/TUS0217108
 GENERAL INFORMATION:
 APPLICANT: Cytovia, Inc.
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Nguyen, Bao Ngoc
 APPLICANT: Drewe, John
 APPLICANT: Reddy, P. Sanjeeva
 APPLICANT: Kasibhatla, Shailaja
 APPLICANT: Pervin, Ara
 TITLE OF INVENTION: 4-Substituted-1-(arylmethylidene)thiogemcarbazide and
 TITLE OF INVENTION: 4-Substituted-1-(arylcarbonyl)thiogemcarbazide and
 Analogs as Activators of Caspases and Inducers of
 Apoptosis and the Use Thereof
 FILE REFERENCE: 1735.06OPC01
 CURRENT APPLICATION NUMBER: PCT/US02/17108
 CURRENT FILING DATE: 2002-05-31
 PRIOR APPLICATION NUMBER: US 60/294,641
 PRIOR FILING DATE: 2001-06-01
 NUMBER OF SEQ ID NOS: 1
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fluorogenic substrate
 PCT-US02-17108-1
 Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4
 RESULT 14
 PCT-US02-17486-1
 Sequence 1, Application PC/TUS0217486
 GENERAL INFORMATION:
 APPLICANT: Cytovia, Inc.
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Zhang, Han Zhong
 APPLICANT: Drewe, John
 APPLICANT: Kasibhatla, Shailaja
 TITLE OF INVENTION: Substituted 4-Aryl-3-(3-Aryl-1-Oxo-2-Propenyl)-2(1H)-Quinolinone

TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of Apoptosis and
FILE REFERENCE: 1735.057P01
CURRENT APPLICATION NUMBER: PCT/US02/17486
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/295,007
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO: 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fluorogenic substrate
FEATURE:
NAME/KEY: MCD RES
LOCATION: (1) .(1)
OTHER INFORMATION:
FEATURE:
NAME/KEY: MCD RES
LOCATION: (4) .(4)
OTHER INFORMATION:
PCT-US02-17486-1

RESULT 15
PCT-US02-17892-1
Sequence 1, Application PC/TUS0217892
GENERAL INFORMATION:
APPLICANT: Cytovia, Inc.
APPLICANT: Cai, Sui Xiong
APPLICANT: Zhang, Han Zhong
APPLICANT: Drew, John A.
APPLICANT: Reddy, P. Sanjeeva
APPLICANT: Kasibhatla, Shailaja
APPLICANT: Kuemmerle, Jared Daniel
APPLICANT: Ollis, Kristin P.
TITLE OF INVENTION: Substituted 3-Aryl-5-aryl-[1,2,4]-oxadiazoles and
Title of Invention: Analogs as Activators of Caspases and Inducers of
Title of Invention: Apoptosis and the Use Thereof
FILE REFERENCE: 1735.054PC01
CURRENT APPLICATION NUMBER: PCT/US02/17892
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 60/296,479
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO: 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fluorogenic substrate
PCT-US02-17892-1

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV D
Db 1 DEV D

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OM Protein - protein search, using Sw model

Run on: May 24, 2004, 14:39:07 ; Search time 13.5 Seconds
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Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

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Minimum DB seq length: 0
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Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database : Pending Patents AA New:*

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7: /cggn2_6/prodata/1/paa/US50_NNEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
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2	21	100.0	4	1	PCT-US04-11916-26	Sequence 7, 1 PCT-US04-11916-26
3	21	100.0	4	1	PCT-US04-11915-41	Sequence 7, 1 PCT-US04-11915-41
4	21	100.0	4	1	PCT-US04-11916-23	Sequence 7, 1 PCT-US04-11916-23
5	21	100.0	4	6	US-10-768-976-64	Sequence 6, 1 US-10-768-976-64
6	21	100.0	4	6	US-10-630-926-14	Sequence 14, 1 US-10-630-926-14
7	21	100.0	4	6	US-10-626-905-43	Sequence 43, 1 US-10-626-905-43
8	21	100.0	4	6	US-10-626-258-22	Sequence 22, 1 US-10-626-258-22
9	21	100.0	4	6	US-10-471-720-1	Sequence 1, 1 US-10-471-720-1
10	21	100.0	4	6	US-10-378-1	Sequence 1, 1 US-10-378-1
11	21	100.0	4	6	US-10-263-330A-43	Sequence 1, 1 US-10-263-330A-43
12	21	100.0	4	6	US-10-146-136-1	Sequence 1, 1 US-10-146-136-1
13	21	100.0	4	6	US-10-622-905-43	Sequence 1, 1 US-10-622-905-43
14	21	100.0	4	6	US-10-816-893-1	Sequence 1, 1 US-10-816-893-1
15	21	100.0	4	6	US-10-825-909-41	Sequence 1, 1 US-10-825-909-41
16	21	100.0	4	6	US-10-823-923-23	Sequence 1, 1 US-10-823-923-23
17	21	100.0	4	6	US-10-829-381-5	Sequence 1, 1 US-10-829-381-5
18	21	100.0	4	7	US-60-549-602-4	Sequence 1, 1 US-60-549-602-4
19	21	100.0	5	1	PCT-US04-04752-15	Sequence 1, 1 PCT-US04-04752-15
20	21	100.0	5	6	US-10-684-346-41	Sequence 1, 1 US-10-684-346-41
21	21	100.0	5	6	US-10-684-346-42	Sequence 1, 1 US-10-684-346-42
22	21	100.0	5	6	US-10-829-381-76	Sequence 1, 1 US-10-829-381-76
23	21	100.0	5	6	PCT-US04-11915-42	Sequence 1, 1 PCT-US04-11915-42
24	21	100.0	7	1	PCT-US04-11911-44	Sequence 1, 1 PCT-US04-11911-44
25	21	100.0	7	1	PCT-US04-11916-24	Sequence 1, 1 PCT-US04-11916-24

RESULT 1
 PCT-US03-20668A-1
 Sequence 1, Application PC/TUSS0320668A
 GENERAL INFORMATION:
 APPLICANT: CYTOVIA, INC.
 APPLICANT: CAI, SUI XIONG
 APPLICANT: TSENG, BEN
 APPLICANT: ZHANG, HAN-ZHONG
 APPLICANT: KASITHATA, SHAILAJA
 APPLICANT: OLLIS, KRISTIN P.
 APPLICANT: SIRIMOMA, NILANTHA SUDATH
 APPLICANT: DREWES, JOHN A.
 TITLE OF INVENTION: Derivatives of Gambogic Acid And Analogs As Activators of Caspases and Inducers of Apoptosis
 FILE REFERENCE: 1735-078PC02
 CURRENT APPLICATION NUMBER: PCT/US03-20668A
 PRIORITY FILING DATE: 2003-07-01
 PRIORITY APPLICATION NUMBER: 60/392,358
 PRIORITY FILING DATE: 2003-09-26
 PRIORITY APPLICATION NUMBER: 60/413,649
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 1
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD-RES
 LOCATION: (1)-(1)
 OTHER INFORMATION: N-terminal acetyl
 FEATURE:
 NAME/KEY: MOD-RES
 LOCATION: (4)-(4)
 OTHER INFORMATION: C-terminal N'-ethoxycarbonyl-Rhodamine 110
 PCT-US03-20668A-1

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DB 1 DEVD 4

RESULT 2
 PCT-US04-11915-41
 Sequence 41, Application PC/TUSS0411915
 ; Sequence 41, Application PC/TUSS0411915

GENERAL INFORMATION:
 APPLICANT: Kasibhatla, Shailaja
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Tseng, Ben
 APPLICANT: Jossen, Karyoun Alayi
 APPLICANT: English, Nicolle Marion
 APPLICANT: Mairachouk, Serguei
 APPLICANT: Jiang, Songshun
 APPLICANT: Sirisoma, Nilantna Sudath
 APPLICANT: Zhang, Han-Zhong
 APPLICANT: Kuemmerle, Jared
 APPLICANT: Cytovia, Inc.
 TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
 TITLE OF INVENTION: and Screening Assays
 FILE REFERENCE: 1735.087PC01
 CURRENT FILING DATE: 2004-04-23
 PRIOR APPLICATION NUMBER: US 60/484,750
 PRIOR FILING DATE: 2003-07-07
 PRIOR APPLICATION NUMBER: US 60/463,549
 PRIOR FILING DATE: 2003-04-18
 PRIOR APPLICATION NUMBER: US 60/532,665
 PRIOR FILING DATE: 2003-12-29
 PRIOR APPLICATION NUMBER: US 60/463,662
 PRIOR FILING DATE: 2003-04-18
 PRIOR APPLICATION NUMBER: US 60/484,749
 PRIOR FILING DATE: 2003-07-07
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 41
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic Peptide
 PCT-US04-11915-41

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 3
 PCT-US04-11916-23
 Sequence 23, Application PC/TUS04-11916
 GENERAL INFORMATION:
 APPLICANT: Kasibhatla, Shailaja
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Jossen, Karyoun Alayi
 APPLICANT: Mairachouk, Serguei
 APPLICANT: English, Nicolle Marion
 APPLICANT: Klemmitzer, William E.
 APPLICANT: Zhang, Han-Zhong
 APPLICANT: Kuemmerle, Jared
 APPLICANT: Cytovia, Inc.
 TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
 TITLE OF INVENTION: and Screening Assays
 FILE REFERENCE: 1735.087PC01
 CURRENT FILING DATE: 2004-04-23
 PRIOR APPLICATION NUMBER: PCT/US04/11916
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 23
 LENGTH: 4
 TYPE: PRT

Query Match 100.0%; Score 21; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 4
 US-10-768-976-64
 Sequence 64, Application US/10768976
 GENERAL INFORMATION:
 APPLICANT: Wood, Keith V.
 APPLICANT: Los, Georgyi V.
 APPLICANT: Bulliet, Robert F.
 APPLICANT: Klausbert, Dietter
 APPLICANT: McDougall, Mark
 APPLICANT: Zimprich, Chad
 APPLICANT: Promega Corporation.
 TITLE OF INVENTION: Covalent Tethering of Functional Groups to Proteins
 FILE REFERENCE: 341.020US1
 CURRENT APPLICATION NUMBER: US/10/768,976
 CURRENT FILING DATE: 2004-01-30
 PRIOR APPLICATION NUMBER: US 60/444,094
 PRIOR FILING DATE: 2003-01-31
 PRIOR APPLICATION NUMBER: US 60/474,659
 PRIOR FILING DATE: 2003-05-30
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 64
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: A synthetic peptide
 US-10-768-976-64

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 5
 US-10-630-926-14
 Sequence 14, Application US/10630926
 GENERAL INFORMATION:
 APPLICANT: RICCARDI, Carlo
 TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
 DEATH PATHWAYS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESS: BRONY AND NETMARK, P.L.L.C.
 STREET: 624 Ninth Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/630,926
 FILING DATE: 31-Jul-2003
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/403,861A
 FILING DATE: 11-Feb-2000
 APPLICATION NUMBER: PCT/BP98/02490
 FILING DATE: 27-APR-1998
 APPLICATION NUMBER: EP 97107033.9
 FILING DATE: 28-APR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: YUN, Allen C.
 REGISTRATION NUMBER: 37,971
 REFERENCE/DOCKET NUMBER: RICCARIDI=1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-624-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FEATURE:
 OTHER INFORMATION: /note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-2-moronyl-7-amide)"
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 us-10-630-926-14

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 6
 US-10-626-905-43
 Sequence 43, Application US/10626905
 GENERAL INFORMATION:
 APPLICANT: FRANZOZO, GUIDO
 APPLICANT: DESMABLE, ENRICO
 APPLICANT: ZAZZERONI, FRANCESCA
 APPLICANT: PAPA, SALVATORE
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS
 FILE REFERENCE: 21459-94575
 CURRENT APPLICATION NUMBER: US/10/626,905
 CURRENT FILING DATE: 2003-07-25
 PRIOR APPLICATION NUMBER: PCT/US02/31548
 PRIOR FILING DATE: 2002-10-02
 PRIOR APPLICATION NUMBER: 10/263,330
 PRIOR FILING DATE: 2002-10-02
 PRIOR APPLICATION NUMBER: 60/328,811
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/326,492
 PRIOR FILING DATE: 2001-10-02
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 43

Length: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 us-10-626-905-43

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 7
 US-10-626-258-22
 Sequence 22, Application US/10626258
 GENERAL INFORMATION:
 APPLICANT: Snarely, Marshall
 APPLICANT: Kliansky, Lena
 TITLE OF INVENTION: Enhanced Solubility of Recombinant Proteins
 FILE REFERENCE: A-725
 CURRENT APPLICATION NUMBER: US/10/626,258
 CURRENT FILING DATE: 2003-07-23
 PRIOR APPLICATION NUMBER: US/09/715,521C
 PRIOR FILING DATE: 2000-11-17
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 22
 LENGTH: 4
 TYPE: PRT
 ORGANISM: caspase 3 protease
 us-10-626-258-22

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 8
 US-10-471-720-1
 Sequence 1, Application US/10471720
 GENERAL INFORMATION:
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Reedy, E. Sanjeeva
 APPLICANT: Drewe, John A.
 APPLICANT: Nguyen, Bao Ngoc
 APPLICANT: Kasibhatla, Shailla
 TITLE OF INVENTION: Multifluoro-substituted Chalcones and Analogs as Activators of Caspases and Inducers of Apoptosis and the Use Thereof
 FILE REFERENCE: 1735-054001
 CURRENT APPLICATION NUMBER: US/10/471,720
 CURRENT FILING DATE: 2003-09-15
 PRIOR APPLICATION NUMBER: PCT/US02/07569
 PRIOR FILING DATE: 2002-03-14
 PRIOR APPLICATION NUMBER: US 60/275,473
 PRIOR FILING DATE: 2001-03-14
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fluorogenic substrate
 us-10-471-720-1

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 9
 US-10-030-378-1

Sequence 1; Application US/10030378
 GENERAL INFORMATION:
 APPLICANT: BLUE, JEFFREY T.
 TITLE OF INVENTION: DETECTION OF VIRAL STABILITY
 FILE REFERENCE: 20455P
 CURRENT FILING DATE: 2001-11-09
 PRIOR APPLICATION NUMBER: US/10/030,378
 PRIOR FILING DATE: 2000-05-10
 PRIOR APPLICATION NUMBER: 60/134,163
 PRIOR FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: caspase 3 substrate

Query Match Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DEVD 4
Db	1 DEVD 4

RESULT 10
 US-10-263-330A-43
 Sequence 43; Application US/10263330A
 GENERAL INFORMATION:
 APPLICANT: FRANZOZO, GUIDO
 APPLICANT: DESMAELE, ENRICO
 APPLICANT: ZAZZERONI, FRANCESCA
 APPLICANT: PAPA, SALVATORE
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS
 FILE REFERENCE: 21459-93823
 CURRENT APPLICATION NUMBER: US/10/263,330A
 CURRENT FILING DATE: 2002-10-02
 PRIOR APPLICATION NUMBER: 60/328,811
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/326,492
 PRIOR FILING DATE: 2001-10-02
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO: 43
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-10-263-330A-43

Query Match Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DEVD 4
Db	1 DEVD 4

RESULT 11-
 US-10-146-136-1
 Sequence 1; Application US/10146136
 GENERAL INFORMATION:
 APPLICANT: CAI, SUI XIONG
 APPLICANT: ZHANG, HONG
 APPLICANT: KENNITZER, WILLIAM

APPLICANT: DREW, JOHN A.
 APPLICANT: STORE, RICHARD
 TITLE OF INVENTION: SUBSTITUTED COUMARINS AND QUINOLINES AND ANALOGS AS ACTIVATORS OF CASPASES AND INDUCERS OF APOPTOSIS AND THE USE THEREOF
 FILE REFERENCE: 1735-0060001
 CURRENT APPLICATION NUMBER: US/10/146,136
 CURRENT FILING DATE: 2002-05-16
 PRIOR APPLICATION NUMBER: 60/290,978
 PRIOR FILING DATE: 2001-05-16
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Fluorogenic substrate
 US-10-146-136-1

Query Match Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DEVD 4
Db	1 DEVD 4

RESULT 12
 US-10-626-905A-43
 Sequence 43; Application US/10626905A
 GENERAL INFORMATION:
 APPLICANT: FRANZOZO, GUIDO
 APPLICANT: DESMAELE, ENRICO
 APPLICANT: ZAZZERONI, FRANCESCA
 APPLICANT: PAPA, SALVATORE
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS
 FILE REFERENCE: 21459-94575
 CURRENT APPLICATION NUMBER: US/10/626,905A
 CURRENT FILING DATE: 2003-07-15
 PRIOR APPLICATION NUMBER: PCT/US02/31548
 PRIOR FILING DATE: 2002-10-02
 PRIOR APPLICATION NUMBER: 10/263,330
 PRIOR FILING DATE: 2002-10-02
 PRIOR APPLICATION NUMBER: 60/328,811
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/326,492
 PRIOR FILING DATE: 2001-10-02
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO: 43
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-10-626-905A-43

Query Match Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DEVD 4
Db	1 DEVD 4

RESULT 13
 US-10-816-893-1
 Sequence 1; Application US/10816893
 GENERAL INFORMATION:

APPLICANT: Cai, Sui Xiong
 APPLICANT: Kasibhatla, Shailaja
 APPLICANT: Dreve, John
 APPLICANT: Reddy, P. Sanjeeva
 APPLICANT: Zhang, Han-Zhong
 TITLE OF INVENTION: Substituted N'-(Arylcarbonyl)-Benzhydrazides And Analogs As Activators Of Caspases And Inducers Of Apoptosis And The Use Thereof
 FILE REFERENCE: 1735-0560002
 CURRENT APPLICATION NUMBER: US/10/816,893
 CURRENT FILING DATE: 2004-04-05; Length 4;
 PRIOR APPLICATION NUMBER: US 10/141,769
 PRIOR FILING DATE: 2002-05-10
 PRIOR APPLICATION NUMBER: US 60/289,803
 PRIOR FILING DATE: 2001-05-10
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Fluorogenic substrate
 US-10-816-893-1

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 14
 US-10-826-909-41
 Sequence 41, Application US/10826909
 GENERAL INFORMATION:
 APPLICANT: Kasibhatla, Shailaja
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Tseng, Ben
 APPLICANT: Jessen, Katayoun Alavi
 APPLICANT: Maliartchouk, Serguei
 APPLICANT: English, Nicole Marion
 APPLICANT: Kuemmerle, Jared
 APPLICANT: Kennitter, William E.
 APPLICANT: Zhang, Han-Zhong
 APPLICANT: Kuemmerle, Jared
 TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
 TITLE OF INVENTION: and Screening Assays
 FILE REFERENCE: 1735-0870001
 CURRENT APPLICATION NUMBER: US/10/826,923
 CURRENT FILING DATE: 2004-04-19
 PRIOR APPLICATION NUMBER: 60/463,687
 PRIOR FILING DATE: 2003-04-18
 NUMBER OF SEQ ID NOS: 31
 SEQ ID NO 23
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic Peptide
 US-10-826-923-23

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

RESULT 15
 US-10-826-923-23
 Sequence 23, Application US/10826923
 GENERAL INFORMATION:
 APPLICANT: Kasibhatla, Shailaja
 APPLICANT: Cai, Sui Xiong
 APPLICANT: Tseng, Ben
 APPLICANT: Jessen, Katayoun Alavi
 APPLICANT: Maliartchouk, Serguei
 APPLICANT: English, Nicole Marion
 APPLICANT: Kuemmerle, Jared
 APPLICANT: Kennitter, William E.
 APPLICANT: Zhang, Han-Zhong
 APPLICANT: Kuemmerle, Jared
 TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
 TITLE OF INVENTION: and Screening Assays
 FILE REFERENCE: 1735-0870001
 CURRENT APPLICATION NUMBER: US/10/826,923
 CURRENT FILING DATE: 2004-04-19
 PRIOR APPLICATION NUMBER: 60/463,687
 PRIOR FILING DATE: 2003-04-18
 NUMBER OF SEQ ID NOS: 31
 SEQ ID NO 23
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic Peptide
 US-10-826-923-23

Query Match 100.0%; Score 21; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 1 DEVD 4

TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis

FILE REFERENCE: 1735-0870001

CURRENT APPLICATION NUMBER: US/10/826,909

CURRENT FILING DATE: 2004-04-19

PRIOR APPLICATION NUMBER: US 60/484,750

PRIOR FILING DATE: 2003-07-07

PRIOR APPLICATION NUMBER: US 60/463,649

PRIOR FILING DATE: 2003-04-18

PRIOR APPLICATION NUMBER: US 60/532,665

PRIOR FILING DATE: 2003-12-29

PRIOR APPLICATION NUMBER: US 60/463,662

PRIOR FILING DATE: 2003-04-18

PRIOR APPLICATION NUMBER: US 60/484,749

PRIOR FILING DATE: 2003-07-07

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.2

SEQ ID NO 41

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-10-826-909-41

Search completed: May 24, 2004, 14:48:20

Job time : 13.5 SECs

B43714 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - *Pseudomonas* sp. (fragment)
 C;Species: *Pseudomonas* sp.
 C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 26-May-2000
 C;Accession: B43714
 R;Anderson, D.H.; Rodewell, V.W.
 J;Bacteriol, 171, 668-672, 1989
 A;Title: Nucleotide sequence and expression in *Escherichia coli* of the 3-hydroxy-3-methyl glutaryl-CoA reductase gene from *Pseudomonas jannaschii*
 A;Reference number: A43714; MUID:9008056; PMID:2687236
 A;Accession: B43714
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-44 <AND>
 A;Cross references: GB:M31807; NID:9151370; PIDN:AAA25894.1; PID:9151371
 C;Superfamily: Methanococcus jannaschii hydroxymethylglutaryl-CoA reductase (NADPH)
 C;Keywords: coenzyme A; oxidoreductase

Query Match 100.0%; Score 21; DB 2; Length 44;
 Best Local Similarity 100.0%; Fred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 14 DEVD 17

RESULT 4
 D95155 hypothetical protein SP1339 [imported] - *Streptococcus pneumoniae* (strain TIGR4)
 C;Species: *Streptococcus pneumoniae*
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 2001-08-03
 C;Accession: D95155
 R;Retetilin, H.; Neilson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidnson, T.; Umayam, L.A.; White, C.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle, S.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001.
 A;Authors: Loftus, B.J.; Yang, F.; Smith, R.O.; Ventresca, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A550000; MUID:21357209; PMID:11463916
 A;Accession: D95155
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-45 <KUR>
 A;Cross-references: GB:AE005672; PIDN:AAK75437.1; PID:914972822; GSPDB:GN00164; TIGR:SP4
 A;Experimental source: strain TIGR4
 C;Genes: SPI339

Query Match 100.0%; Score 21; DB 2; Length 45;
 Best Local Similarity 100.0%; Fred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 19 DEVD 22

RESULT 5
 T21746 hypothetical protein P35C12.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T21746
 R;Baynes, C.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z19468
 A;Accession: T21746
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-49 <WIL>
 A;Cross-references: EMBL:Z81075; PIDN:CA03046.1; GSPDB:GN00019; CESP:F35C12.1
 A;Experimental source: clone F35C12
 C;Genetics:

A;Gene: CESP:F35C12.1
 A;Map position: 1
 A;Introns: 15/2
 Query Match 100.0%; Score 21; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 33 DEVD 36

RESULT 6
 DQ0129 34.5K linker protein - *Fischerella* sp. (fragment)
 C;Species: *Fischerella* sp.
 C;Accession: DQ0129
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-Jan-2000
 C;Accession: DQ0129
 R;Eberlein, M.; Kufer, W.
 Gene 94, 133-136, 1990
 A;Title: Genes encoding both subunits of phycoerythrocyanin, a light-harvesting biliprotein
 A;Reference number: JQ0163; MUID:9103055; PMID:2121619
 A;Accession: PC0129
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-58 <EBE>
 A;Cross-references: GB:M34254
 C;Superfamily: phycocyanin linker protein cpCH3

Query Match 100.0%; Score 21; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 13 DEVD 16

RESULT 7
 C69169 hypothetical protein MTH525 - *Methanobacterium thermoautotrophicum* (strain Delta H)
 C;Species: *Methanobacterium thermoautotrophicum*
 C;Accession: C69169
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Ies, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vacaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: func
 A;Reference number: A69000; MUID:98C37514; PMID:9371463
 A;Accession: C69169
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-10 <MTH>
 A;Cross-references: GB:AE00835; GB:AE00666; PIDN:AAB85031.1; PID:g2621586;
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH525

Query Match 100.0%; Score 21; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 22 DEVD 25

RESULT 8
 T17388 vRL protein - *Dichelobacter nodosus*
 C;Species: *Dichelobacter nodosus*

C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C; Accession: T17388
 R; Billington, S.J.; Huggins, A.S.; Johansen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, N.
 Infect Immun 67, 1277-1286, 1999
 A; Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) c
 A; Reference number: 218734; MUID:9150261; PMID:10024571
 A; Accession: T17388
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-67 <BT>
 A; Cross-references: EMBL:U20246; NID:G34933233; PID:93482870; PIDN:AAC33397.1
 A; Experimental source: strain A198

Query Match Score 21; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0;

Qy 1 DEVD 4
 Db 47 DEVD 50

RESULT 11
 H81078
 4-oxalocrotonate tautomerase (EC 5.3.2.-) NMB1474 [similarity] - Neisseria meningitidis
 C; Species: Neisseria meningitidis
 C; Accession: H81078; H1863
 C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
 R; Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, L.; Hickie, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.; Fier, H.; Qin, H.; Yamane, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A; Reference number: A81000; MUID:20175755; PMID:10710307
 A; Accession: H81078
 A; Molecule type: DNA
 A; Residues: 1-69 <TET>
 A; Cross-references: GB:AE002497; GB:AB00298; NID:97226712; PIDN:AAF41831.1; PID:97226712
 A; Experimental source: serogroup B, strain MC58
 R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Kles, S.R.; Mori, I.; Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandes
 Nature 404, 502-506, 2000
 A; Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A; Reference number: A81775; MUID:2022556; PMID:10761919
 A; Accession: H81078
 A; Molecule type: DNA
 A; Residues: 1-69 <PAR>
 A; Cross-references: GB:AL162756; GB:AL157959; NID:97380091; PIDN:CAB84913.1; PID:97380091
 A; Experimental source: serogroup A, strain Z2491
 C; Genetics:

A; Gene: Jhp0858
 C; Superfamily: 4-oxalocrotonate tautomerase
 C; Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase
 R; F2'-6'Product: 4-oxalocrotonate tautomerase
 P; /Active site: Pro #status Predicted

Query Match Score 21; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0;

Qy 1 DEVD 4
 Db 47 DEVD 50

RESULT 10
 D64635
 4-oxalocrotonate tautomerase (EC 5.3.2.-) HPP0924 [similarity] - Helicobacter pylori (str
 C; Species: Helicobacter pylori
 C; Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 17-Mar-2000
 C; Accession: D64635
 R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, R.D.; Sod, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watchey, L.; Nature 388, 539-547, 1997
 A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.; A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A; Reference number: A84520; MUID:9794467; PMID:952155
 A; Accession: D64635
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-68 <TOM>

A; Cross-references: GB:AE000602; GB:AE000511; NID:92314060; PIDN:AAD07977.1; PID:92314
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 C; Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase
 R; F2'-6'Product: 4-oxalocrotonate tautomerase #status Predicted <MAT>
 P; /Active site: Pro #status Predicted

Query Match Score 21; DB 2; Length 68;
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 Matches 4; Conservative 0;

Qy 1 DEVD 4
 Db 47 DEVD 50

RESULT 11
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 4-oxalocrotonate tautomerase (EC 5.3.2.-) NMB1474 [similarity] - Neisseria meningitidis
 C; Species: Neisseria meningitidis
 C; Accession: H81078; H1863
 R; Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, L.; Hickie, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.; Fier, H.; Qin, H.; Yamane, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A; Reference number: A81000; MUID:20175755; PMID:10710307
 A; Accession: H81078
 A; Molecule type: DNA
 A; Residues: 1-69 <TET>
 A; Cross-references: GB:AE002497; GB:AB00298; NID:97226712; PIDN:AAF41831.1; PID:97226712
 A; Experimental source: serogroup B, strain MC58
 R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Kles, S.R.; Mori, I.; Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandes
 Nature 404, 502-506, 2000
 A; Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A; Reference number: A81775; MUID:2022556; PMID:10761919
 A; Accession: H81078
 A; Molecule type: DNA
 A; Residues: 1-69 <PAR>
 A; Cross-references: GB:AL162756; GB:AL157959; NID:97380091; PIDN:CAB84913.1; PID:97380091
 A; Experimental source: serogroup A, strain Z2491
 C; Genetics:

A; Gene: NMB1474; NMA1685
 C; Superfamily: 4-oxalocrotonate tautomerase
 C; Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase
 R; F2'-6'Product: 4-oxalocrotonate tautomerase #status Predicted <MAT>
 P; /Active site: Pro #status Predicted

Query Match Score 21; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0;

Qy 1 DEVD 4
 Db 47 DEVD 50

RESULT 12
 E82829
 hypothetical protein XF2242 [imported] - Xylella fastidiosa (strain 9a5c)
 C; Species: Xylella fastidiosa
 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C; Accession: E82829
 R; Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
 Nature 406, 151-157, 2000
 A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A; Reference number: A82515; MUID:20385717; PMID:10910347
 A; Note: for a complete list of authors see reference number A59328 below
 A; Accession: E82829

A; Status: Preliminary
A; Molecule type: DNA
A; Residues 1-74 <SIM>
A; Experimental source: strain 9a5c
A; Cross-references: GB:AE003849; PIDN:BA83055.1; GSPDB:GN00154
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; Briones, M.R.P.; Bueno, M.R.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer, P.; Neto, E.; Docaia, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, J.C.A.; Ferro, J.A.; Fraaga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, M.A.; Madeira, B.L.; Kempfer, B.L.; Kittijima, J.P.; Krieger, J.B.; Kuramae, E.B.; Laing, F.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Menck, C.F.M.; Marino, C.L.; Martins, E.; Rodriguez, V.; Rossa, A.J.; de Rosa Jr., V.E.; de Souza, R.G.; Santelli, R.V.; Sawada, M.; Tsuchako, M.H.; Vallada, H.; Van Siuys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A; Reference number: A59328
A; Content: annotation
C; Genetics:
A; Gene: XP02422
Query Match 100.0%; Score 21; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 64 DEVD 67
RESULT 13

F64032 hypothetical protein HI1497 - Haemophilus influenzae (strain Rd KW20)
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C; Accession: F64032
R; Fleisschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Gooley, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Gocayne, J.D.; Weilman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Science 265, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.A.; Reference number: A64000; PMID:95350630; PMID:7542800
A; Accession: F64032
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-75 <TRGR>
A; Cross-references: GB:U12826; GB:L142023; PIDN:AAC21137.1; PIDN:91574327; T

Query Match 100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEVD 4
Db 31 DEVD 34

RESULT 14

D91267 hypothetical protein EC55108 [imported] - Escherichia coli (strain O157:H7, substrain RI)
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Accession: D91267
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A; Reference number: A99629; PMID:21156231; PMID:11258796
A; Accession: D91267
A; Status: preliminary
A; Molecule type: DNA

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OM protein - protein search, using SW model

Run on: May 24, 2004, 14:36:17 ; Search time 10.5 Seconds

(without alignments)

19.836 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SwissProt_42.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Score Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	21	100.0	20	1	FIBB_SHEEP	P14470;	
2	21	100.0	21	1	FIBB_ODOHE	AC	
3	21	100.0	60	1	Y060_BRAJA	DT 01-JAN-1990 (Rel. 13, Created)	
4	21	100.0	63	1	MIP_BOTPU	DT 01-JAN-1990 (Rel. 13, Last sequence update)	
5	21	100.0	67	1	Y058_HELPY	DT 10-OCT-2003 (Rel. 42, Last annotation update)	
6	21	100.0	67	1	Y924_HELPY	DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).	
7	21	100.0	75	1	Y097_HAEIN	GN FGB.	
8	21	100.0	76	1	Y0DI_ECOLI	P36198 saccharomyces cerevisiae YKA2_YERST	
9	21	100.0	77	1	M05A_AMBPS	P36198 saccharomyces cerevisiae YKA2_YERST	
10	21	100.0	88	1	E01B_THEAC	P36198 saccharomyces cerevisiae YKA2_YERST	
11	21	100.0	95	1	L0M2_HUMAN	P36198 saccharomyces cerevisiae YKA2_YERST	
12	21	100.0	97	1	VE7 HPV44	P36198 saccharomyces cerevisiae YKA2_YERST	
13	21	100.0	97	1	VE7 HPV55	P36198 saccharomyces cerevisiae YKA2_YERST	
14	21	100.0	97	1	Y079_METJU	P36198 saccharomyces cerevisiae YKA2_YERST	
15	21	100.0	98	1	VE7 HPV11	P04020 human papillomavirus type 11	
16	21	100.0	98	1	VE7 HPV6A	Q829292 human papillomavirus type 6	
17	21	100.0	98	1	VE7 HPV6B	P06664 human papillomavirus type 6	
18	21	100.0	98	1	VE7 PCPVL	Q02272 pygmy chimpanzee papillomavirus	
19	21	100.0	101	1	GATC_LACLA	Q9C144 lactococcus lactis subsp. lactis	
20	21	100.0	101	1	VE7 HPV13	Q02271 human papillomavirus type 13	
21	22	100.0	101	1	VE7 HPV51	P26558 human papillomavirus type 51	
22	21	100.0	105	1	DBH_TREPA	Q83278 treponema pallidum subsp. pallidum	
23	21	100.0	105	1	GNNI_NETTL	P25771 methanococcus jannaschii nettl	
24	21	100.0	105	1	VE7 HPV50	P36326 human papillomavirus type 50	
25	21	100.0	105	1	VE7 HPV53	P36332 human papillomavirus type 53	
26	21	100.0	105	1	VE7 HPV56	P36333 human papillomavirus type 56	
27	21	100.0	113	1	CHAV_RALSO	Q8X554 ralstonia eutropha	
28	21	100.0	113	1	VE7 HPV1	P22161 rhesus papio	
29	21	100.0	119	1	PSIC_ECOLI	P23055 escherichia coli	
30	21	100.0	129	1	YS11_CABEL	Q102020 caenorhabditis elegans	
31	21	100.0	133	1	ATPE_MCGE	P47838 mycoplasma genitalium	
32	21	100.0	135	1	RSE_EHALMA	P21109 haloarcula	
33	21	100.0	138	1	YFPO_ECOLI	P76546 escherichia coli	

ALIGNMENTS

RESULT 1						
FB	B	S	H	P	R	T
FIBB_SHEEP	SHEEP	STANDARD;				
ID						
AC						
P14470;						
DT						
01-JAN-1990 (Rel. 13, Created)						
DT						
01-JAN-1990 (Rel. 13, Last sequence update)						
DT						
10-OCT-2003 (Rel. 42, Last annotation update)						
DE						
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).						
GN						
FGB.						
OS						
SEQUENCE						
"Studies on fibrinopeptides from mammals."						
RA						
Blomback B., Blomback M., Grondahl N.J./						
RT						
Acta Chem. Scand. 19:1789-1791 (1965).						
CC						
-: FUNCTION: Fibrinogen has a double function: yielding monomers that						
CC						
polymerize into fibrin and acting as a coactor in platelet						
CC						
-: AGGREGATION:						
CC						
-: PROTEIN: Hexamer containing 2 sets of 3 nonidentical chains						
CC						
(alpha, beta and gamma), linked to each other by disulfide bonds.						
CC						
-: PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,						
CC						
which cleaves fibrinopeptides A and B from alpha and beta chains						
CC						
and thus exposes the N-terminal polymerization sites responsible						
CC						
for the formation of the soft clot.						
DR						
PROSITE; PS00314; FIBRIN_AGC_DOMAIN; PARTIAL.						
KW						
BLOOD COAGULATION; PLASMA; SULFATION.						
FT						
PEPTIDE 1						
FT						
MOD_RES 5						
FT						
NON_TER 20						
SQ						
SEQUENCE 20 AA; MW; FCFSB6FFODEG6627 CRC64;						
Qy						
Query Match 100.0%; Score 21; DB 1; Length 20;						
Best Local Similarity 100.0%; Pred. No. 44; Mismatches 0; Indels 0; Gaps 0;						
DB						
1 DEV0 4						
6 DEV0 9						

RESULT 2						
FB	B	S	H	P	R	T
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ID						
P14476						
AC						
01-JAN-1990 (Rel. 13, Created)						
DT						
01-FEB-1994 (Rel. 28, Last sequence update)						
DT						
10-OCT-2003 (Rel. 42, Last annotation update)						
DE						
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).						
GN						
FGB.						
OS						
Odocoileus hemionus (Mule deer) (Black-tailed deer).						

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
 Cervidae; Odocoileinae; Odocoileus.
 NCBT_TaxID=9872;
 [1] P
 SEQUENCE
 MEDLINE=67209145; PubMed=6033721;
 Doolittle R.F., Schubert D., Schwartz S.A.; "Amino acid sequence studies on arriodactyl fibrinopeptides. I. Dromedary camel, mule deer, and cape buffalo.," Arch. Biochem. Biophys. 118:456-467(1967).
 -:!- FUNCTION: Fibrinogen has a double function: Yielding monomers that polymerize into fibrin and acting as a cofactor in Platelet aggregation.
 -:!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 -:!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
 InterPro: IPR002181; Fibrinogen C.
 PROSITE: PS00514; FIBIN AG C DOMAIN; PARTIAL.
 BLOOD COAGULATION; PLASMA_Sulfation; Pyrrolidone carboxylic acid.
 PEPTIDE 21 Pyrrolidone carboxylic acid.
 MOD RES 1 1
 MOD RES 6 6
 NON-TER 21 21
 SEQUENCE 21 AA; 2496 MW; FCF562G51A001627 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 DEVD 4
 |||||
 7 DEVD 10
 b
 RESULT 3
 C60-BRAJA STANDARD; PRT; 60 AA.
 D YC60-BRAJA STANDARD; PRT; 60 AA.
 C Q89UZ9;
 T 10-OCT-2003 (Rel. 42, Created)
 T 10-OCT-2003 (Rel. 42, Last sequence update)
 T 10-OCT-2003 (Rel. 42, Last annotation update)
 T Hypothetical zinc-binding UPF0243 protein bsr1260
 BSR1260.
 Bradyrhizobium japonicum.
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Bradyrhizobiaceae; Bradyrhizobium.
 NCBI_TaxID=375;
 [1] N
 SEQUENCE FROM N.A.
 STRAIN=UDA 110;
 MEDLINE=2249998; PubMed=12597225;
 Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasaki S., Watanabe A., Idezawa K., Iriuchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.,
 "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110," DNA Res. 9:183-197(2002).
 -:!- COFACTOR: Binds 1 zinc ion (By similarity).
 -:!- SIMILARITY: Belongs to the UPF0243 family.
 l
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 C

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DR EMBL; AP005939; BAC46525.1; -
DR HAMAP; MF_00649; -; 1.
DR InterPro; IPR005584; DUF329.
DR Pfam; PF03884; DUF329; 1.
KW Hypothetical protein; Zinc; Metal-binding; Complete proteome.
FT METAL 15 21NC (BY SIMILARITY).
FT METAL 18 18 ZINC (BY SIMILARITY).
FT METAL 30 30 ZINC (BY SIMILARITY).
FT METAL 34 34 ZINC (BY SIMILARITY).
SQ SEQUENCE 60 AA; 6532 MN; CD55FFEB0278B1D9 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0

Qy 1 DEVD 4
Db 54 DEVD 57

RESULT 4
MIP_BOTAS STANDARD; PRT; 63 AA.
ID MIP_BOTAS
AC P61077;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DB Myotoxin inhibitor Protein MIP.
OS Bothrops asper (Terciopelo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
Lepidosaurs; Squamata; Scleroglossa; Sepientes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OC NCBITaxonID=8722;
RN 11
RP RP
SEQUENCE.
TISSUE=Blood;
RX MEDLINE=9439529; PubMed=9307037;
RA Lizano S.; Lomonte B.; Fox J.W.; Gutierrez J.M. ;
RT "Biochemical characterization and pharmacological properties of the snake phospholipase A2 myotoxin inhibitor from the plasma of the snake Bothrops asper"; RT Biochem. J. 326:853-859 (1997).
CC -- PUNCTUATION: Binds to and neutralizes the activities of basic phospholipase A2 (PLA2) myotoxin isoforms.
CC -- SUBUNIT: Oligomer composed of five 23-25 kDa subunits.
CC -- SUBCELLULAR LOCATION: Secreted.
CC -- SIMILARITY: Contains 1 C-type lectin family domain.
KW Glycoprotein; Plasma; Lectin.
SQ SEQUENCE 63 AA; 7154 MW; FIE6AF75D8489CB6 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0

Qy 1 DEVD 4
Db 54 DEVD 4

RESULT 5
Y858_HELPPU STANDARD; PRT; 67 AA.
ID Y858_HELPPU
AC Q9ZKS7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable tautomerase (EC 5.3.2.-).
DE JP08588.
GN Helicobacter pylori J99 (Campylobacter pylori J99).
OS Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacter.
OC Helicobacteraceae; Helicobacter.
OC NCBITaxonID=85963;
RN

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SEQUENCE FROM N.A. PubMed=9923682; RX MEDLINE=9120557; King B.L., Brown B.D., Doig P.C., RA Alm R.A., Ling L.-S.L., Moir D.T., Guild B.C., deJonge B.L., Carmel G., Smith D.R., Nevanon B., Guild B.C., deJonge B.L., Carmel G., Tummino M., Uriya-Nickel M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.; RT "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen *Helicobacter pylori*."; RT RL 39:176-180(1999).

CC |- SIMILARITY: Belongs to the tautomerase family.

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CC EMBL: AE001515; AA006434.1; -.

DR PIR; B71880; B71880;

DR HAMAP; MF_00718; -; 1.

DR InterPro; IPR004370; Tautomerase;

DR Pfam; PF03361; Tautomerase; 1.

DR ProDom; PR0404143; Taut; 1.

DR TIGRFAMS; TIGR00013; taut; 1.

KW Isomerase; Complete proteome;

INIT_MER 0 BY SIMILARITY.

FT ACT SITE 0 CATALYTIC BASE (BY SIMILARITY).

FT SEQ 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 46 DEVD 49

RESULT 6 CATALYTIC BASE (BY SIMILARITY).

FT ACT SITE 1 7394 MN; F5AD98AA31A739FB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 67;

</

PRINTS; PR00618; DK5AZNFINGER; 1.
DR PROSITE; P0110; DK5A-TRARZN_FINGER; Zinc-Finger/ Complete Proteome.
KW Hypothetical protein; Zinc-Finger.
FT ZN FING 43 67 TRAR/DKSA-TYPE
SEQUENCE 75 AA; 84.05 MW; 9F6DAD6F2C02C626 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 31 DEVD 34

RESULT 8
YJDI_ECOLI ID YJDI_ECOLI STANDARD; PRT; 76 AA.
AC P3273; DT 01-FEB-1995 (Rel. 31. Created)
DT 01-FEB-1995 (Rel. 31. Last sequence update)
DT 16-OCT-2001 (Rel. 40. Last annotation update)
Hypothetical protein YJDI.
GN YJDI OR B4126 OR Z5738 OR ECSS5108.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteroidales; Escherichia.
OX NCBI_TaxID:566, 83334;
RN RP
SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX M2DLIN=95344362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.,
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100.19 min.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2].
RN SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21104935; PubMed=11205551;
RA Perera N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Grotbeck E.J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533 (2001).

RESULT 9
YJDI_ECOLI ID YJDI_ECOLI STANDARD; PRT; 76 AA.
AC P4374; DT 01-NOV-1995 (Rel. 32. Created)
DT 01-NOV-1995 (Rel. 32. Last sequence update)
DT 10-OCT-2003 (Rel. 42. Last annotation update)
DE Pollen allergen Amb p 5a precursor (Amb p Va).
OS Ambrosia psilostachya (Western ragweed).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Streptophyta; Embryophyta; Tracheophyta;
OC Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Ambrosia.
RN NCBI_TaxID=29715;

RESULT 9
MP5A_AMBPS ID MP5A_AMBPS STANDARD; PRT; 77 AA.
AC P4374; DT 01-NOV-1995 (Rel. 32. Created)
DT 01-NOV-1995 (Rel. 32. Last sequence update)
DT 10-OCT-2003 (Rel. 42. Last annotation update)
DE Pollen allergen Amb p 5a precursor (Amb p Va).
OS Ambrosia psilostachya (Western ragweed).
RN SEQUENCE FROM N.A., AND SEQUENCE OF 23-63.
RC TISSUE=Pollen. RX MEDLINE=94194048; PubMed=7511632;
RA Ghosh B., Rafnar T., Perry M.P., Bassolino-Klimas D.,
RA Metzler W.J., Klapser D.G., Marsh D.G.;
RT "Immunologic and molecular characterization of Amb p V allergens from
RT Ambrosia psilostachya (western Ragweed) pollen.";
RT Immunobiol. 152:288-289(1994).
RL J. Immunol. 152:288-289(1994).
CC -!- ALLERGEN: Causes an allergic reaction in human.

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CC DR EMBL; L24465; AAA20065.1; -.
CC DR EMBL; L24466; AAA20067.1; -.
CC DR HSSP; P1014; IBBG; -.
CC DR InterPro; IPR005611; Amb-V_allergen.
CC DR Pfam; PF03913; Amb_V_allergen; 1.
CC DR PRODOM; PD018550; Amb_V_allergen; 1.
CC DR Allergen; Signal.
CC FT SIGNAL 1 22 POLLEN ALLERGEN AMB P 5A.
CC FT CHAIN 23 77 BY SIMILARITY.
CC FT DISULFID 26 61 BY SIMILARITY.
CC FT DISULFID 33 48 BY SIMILARITY.
CC FT DISULFID 40 54 BY SIMILARITY.
CC FT DISULFID 41 65 BY SIMILARITY.
CC FT VARIANT 59 59 E -> K (IN CLONE A3).
CC SQ SEQUENCE 77 AA; 8710 MW; 2D8376EB65D9A00F CRC64;
CC Query Match Similarity 100.0%; Score 21; DB 1; Length 77;
CC Best Local Similarity 100.0%; Pred. No. 1.7e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 16 DEVD 19

RX	MEDLINE:99432783; PubMed=10523320;	PubMed=10523320;		
RA	Achsel T., Brahm H., Kasner B., Bach A., Wilm M., Luehrmann R.;			
RT	"A doughnut shaped heteromer of human Sm-like proteins binds to the			
RT	3' end of U6 snRNA, thereby facilitating U4/U6 duplex formation in			
RT	EMBO J. 18:5789-5802(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Olaivesa M.G., Campbell R.D.;			
RA	Rowan L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,			
RA	Abbasz N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,			
RA	Lasky S., Hood L.;			
RA	"Characterisation of the novel gene G7b located in the class III			
RT	region of the human major histocompatibility complex.";			
RT	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Rowan L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,			
RA	Abbasz N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,			
RA	Lasky S., Hood L.;			
RA	"Sequence of the human major histocompatibility complex class III			
RT	region."			
RT	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Shihina S., Tamaiya G., Oka A., Inoko H.;			
RA	"Homo sapiens 2,29,817bp genomic DNA of Sp21.3 HLA class I region."			
RT	Submitted (SPR-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=hypothalamus;			
RC	MEDLINE=20402571; PubMed=10931946;			
RA	Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,			
RA	Ru Y.-H., Ruang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,			
RA	Gu B.-W., Dai M., Mao Y.-F., Gao F.-P., Rong R., Ye M., Zhou J.,			
RA	Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,			
RA	Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.			
RA	"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum."			
RT	Nature 407:508-513 (2000).			
CC	-!- FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP, thus allowing the regeneration of EF-1-alpha/GTP that could then be used to form the ternary complex EF-1-alpha/GTP/AAtrNA (By similarity).			
CC	-!- SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.			
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CC	-----			
CC	EMBL; AL445064; CAC11706.1; ALT_INIT.			
DR	HSSP; O77734; 1IGH8.			
DR	HANAP; MF_00043; :-.			
DR	InterPro; IPR004542; aEF-1_beta.			
DR	InterPro; IPR013436; EPI_BD.			
DR	Pfam; PF00736; EP1BD; 1.			
DR	TIGRFAMs; TIGR00489; aEF-1_beta; 1.			
KW	ELONGATION factor; Protein biosynthesis; Complete proteome.			
SEQUENCE	88 AA; 9749 MW; 572357C1BADDEDA7 CRC64;			
Qy	1 DEVD 4 40 DEVD 43			
Db	Best Local Similarity 100.0%; Score 21; DB 1; Length 88; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	STANDARD;			
Db	95 AA.			
RESULTS	11			
ID	LSM2_HUMAN			
OS	Homo sapiens (Human)			
AC	Q9YJ33; AC_09YJ33;			
AC	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	U6 snRNA-associated Sm-like protein Lsm2 (Small nuclear ribonucleic protein D homolog) (G7b) (SmNRP core SM-x5).			
DN	LSM2 OR C6ORE2A OR G7B.			
DN	Homologs (Human)			
OS	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Eukaryota; Metazoa; Primates; Primates; Catarrhini; Hominoidea; Homo.			
NCBI_TaxID	9606;			
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.			
CC	!- SUBUNIT: LSm subunits form a heteromer with a doughtn shape.			
CC	--!- SUBCELLULAR LOCATION: Nuclear (Potential).			
CC	--!- SIMILARITY: Belongs to the SmNRP sm proteins family.			
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CC	!- RNA.			

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CC EMBL; AF182288; AAD56226.1; -.
 DR EMBL; AJ245416; CAB5190_1; -.
 DR EMBL; AF134726; AAD2118_1; -.
 DR EMBL; AP00503; BAB63302.1; -.
 DR EMBL; AF136977; AAG49338.1; -.
 DR EMBL; AF196458; AAG31023.1; -.
 DR EMBL; BC009192; AAH09192.1; -.
 DR GeneID: HGNIC:13940; LEM2.
 DR GK; Q9Y333; -.
 DR MIM; 607282; -.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0017070; F:U6 snRNA binding; NAS.
 DR InterPro; IPR006649; snRNP.
 DR InterPro; IPR001163; snRNP_Sm.
 DR Pfam; PF01423; ISM; 1.
 DR SMART; SM00651; Sm; 1.
 DR SMART; SM00651; Sm; 1.
 KW Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
 KW RNA-binding.
 SQ SEQUENCE 95 AA; 10834 MW; 623591A09AAABACE CRC64;
 Query Match Score 21; DB 1; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DR 75 DEVD 78
 DB

 RESULT 12
 VE7 HPV44 STANDARD; PRT; 97 AA.
 AC Q80514; -.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE E7 protein.
 GN
 OS Human papillomavirus type 44.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 RA Delliush.; /
 RL Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
 CC |- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
 CC ACTIVITIES.
 CC SEQUENCE FROM N.A.
 DR Delliush.; /
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 CC |- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
 CC ACTIVITIES.
 CC SEQUENCE FROM N.A.
 DR Delliush.; /
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 CC |- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
 CC ACTIVITIES.
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SQ SEQUENCE 97 AA; 10641 MW; E4866AE13B050456 CRC64;
 Query Match Score 21; DB 1; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DR 34 DEVD 37
 DB

 RESULT 13
 VE7 HPV55 STANDARD; PRT; 97 AA.
 ID VE7 HPV55
 AC Q80935; -.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE E7 protein.
 GN
 OS Human papillomavirus type 55.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=37114;
 RN [1]
 RP SEQUENCE FROM N.A.
 DR Delliush.; /
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 CC |- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
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DR EMBL; U31791; AAA79379.1; -.
 DR InterPro; IPR000148; Papv1_E7.
 DR Pfam; PF00527; E7; 1.
 KW Early protein; Transcription regulation; Oncogene;
 KW DNA-binding; Trans-acting factor.
 FT SITE 57 60 C-XX-C MOTIF-1.
 FT SITE 90 93 C-XX-C MOTIF-2.
 SQ SEQUENCE 97 AA; 10621 MW; E2937616BCE47D42 CRC64;
 Query Match Score 21; DB 1; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 DR 34 DEVD 37
 DB

 RESULT 14
 YG79_METJA STANDARD; PRT; 97 AA.
 ID YG79_METJA
 AC Q89073; -.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ1679.
 GN
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcaceae;
 OC Methanococcaceae; Methanococcaceae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

DR MEDLINE96337999; PubMed=688087; L36108; ARA21704.1; -

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Fleischmann R.D., Clayton R.A., Clayton R.A., Goedeyne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Tomb J.P., Adams M.D., Geckye C.I., Kerlavage A.R., Dougherty B.A., Tomb J.P., Reich C.I., Overbeek R., Kirchner E.F., Weinstock K.G., Glodek A., Scott J.L., Geesbagen N.S.M., Weidman J.F., Subramanian J.L., Merrick J.M., DNA-banding; Trans-acting factor.

Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Wesse C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii"; Science 273:1073-1076(1996).

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EMBL; U67607; AAB9704.1; -

PIR; E64509; E64509. -

TIGR; MG1679; -

KW Hypothetical protein; Complete proteome.

SEQUENCE 97 AA; 11880 MW; 64C59303B9101FEO CRC64;

Query Match 100.0%; Score 21; DB 1; Length 97; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR MEDLINE96337999; PubMed=688087; L36108; ARA21704.1; -

DR PIR; A03690; W7L111; InterPro; IPR000148; Papv1_E7.

DR PFam; PF00527; E7; 1. DNA-binding; Trans-acting factor.

KW C-XX-C MOTIF-1. C-XX-C MOTIF-2.

FT SITE 58 61

FT SITE 91 94

SO SEQUENCE 98 AA; 10889 MW; AACAS9460C933E1F6 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 98; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 35 DEVD 38

Search completed: May 24, 2004, 14:39:34

Job time : 11.5 secs

RESULT 15

VE7 HPV11 STANDARD; PRT; 98 AA.

VE7 HPV11 ID _VE7 HPV11 AC P04020; 23-OCT-1986 (Rel. 02, Created) 23-OCT-1986 (Rel. 02, Last sequence update)

DE 28-PB-2003 (Rel. 41, Last annotation update)

E7 protein.

E7.

GN Human papillomavirus type 11.

OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Papillomavirus.

OC NCBI_TaxID=10580;

CC [1] RN SEQUENCE FROM N.A. MEDLINE=86181601; PubMed=3008427;

RA Darmann K., Schwarz E., Gissmann L., Zur Hausen H.; "The nucleotide sequence and genome organization of human papilloma virus type 11." Virology 151:124-130(1986).

CC [2] SEQUENCE FROM N.A. Pfe K.H., Fan L., Fritsch M.H., Bryan J., Brown D.R.; Submitted (OCT-1994) to the EMBL Genbank/DBJ databases.

RA - FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING ACTIVITIES.

CC - SIMILARITY: LOCAL WITH ADENOVIRUS E1A AND SV40 LT.

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EMBL; M14119; AAA4928.1; -

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 36.5 Seconds
(without alignments)

34.577 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DVVD 4

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_inhuman:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mic:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_ivirus:*
- 16: sp_bacteriop:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description	
1	21	100.0	11	10	O82070 triticum ae	
2	21	100.0	44	2	Q51913 pseudomonas	
3	21	100.0	45	10	Q49793 arabidopsis	
4	21	100.0	45	16	Q71Q87 streptococc	
5	5	21	100.0	45	16	Q8FVIL6 brucella su
6	21	100.0	49	4	Q56295 homo sapien	
7	21	100.0	49	5	Q9XVP5 caenorhabdi	
8	9	21	100.0	50	11	Q63952 rattus sp.
9	21	100.0	53	13	Q9TAB6	
10	21	100.0	53	16	Q98TMB6	
11	21	100.0	54	9	Q8258 lactococcus	
12	21	100.0	54	9	Q38280	
13	21	100.0	54	10	Q84NR3 oryza sativ	
14	21	100.0	54	17	Q977AO sulfolobus	
15	21	100.0	56	12	Q99H60 human picob	
16	21	100.0	56	12	Q99H57 human picob	

ALIGNMENTS		PRT		PRT; ID		PRELIMINARY; ID		PRELIMINARY; AC		PRELIMINARY; DT		PRELIMINARY; DT		PRELIMINARY; DR		PRELIMINARY; EMBL		PRELIMINARY; NCBI_TaxID=4565;				
Q99H59	human Picob	17	21	100.0	56	12	Q99H59	Q81138	oryza sativ	18	21	100.0	57	10	QBLH38	Q8RJ7	corynebacte	19	21	100.0	57	
Q81138								Q94755	schistosoma	20	21	100.0	59	5	Q94755	Q93AL7	clostridium	21	21	100.0	60	
Q8RJ7								Q7XRA8	oryza sativ	22	21	100.0	60	10	Q7XRA8	Q26625	methanobact	23	21	100.0	60	
corynebacte								Q88K2	rhizobium 1	24	25	21	100.0	62	16	Q88K2	Q83X17	shigella dy	25	21	100.0	63
schistosoma								Q8Pv7	methanoscarc	26	21	100.0	63	17	Q8Pv7	Q83X10	bacteroides	27	21	100.0	65	
clostridium								Q83X13	shigella bo	28	21	100.0	65	13	Q83X13	Q8v86	white spot	29	21	100.0	65	
methanobact								Q8mb4	vibrio vuln	30	21	100.0	66	16	Q8mb4	Q83X7	shigella so	31	21	100.0	66	
Q83X7								Q83X8	shigella dy	32	21	100.0	66	16	Q83X8	Q83X5	neisseria m	33	21	100.0	67	
shigella dy								Q8v6S0	halovirush	34	21	100.0	67	12	Q8v6S0	Q7tD9	halovirush	35	21	100.0	68	
neisseria m								Q9cJQ9	pasteurella	36	21	100.0	69	2	Q9cJQ9	Q83XU0	shigella dy	37	21	100.0	69	
halovirush								Q8v6J0	Q8v6J0	38	21	100.0	69	16	Q8v6J0	Q83XT7	Q83X7	39	21	100.0	70	
Q83X7								Q8v6S0	halovirush	40	21	100.0	70	12	Q8v6S0	Q83XT6	Q83XT6	41	21	100.0	70	
halovirush								Q83XT6	Q83XT6	42	21	100.0	71	2	Q83XT6	Q83XT2	Q83XT2	43	21	100.0	71	
Q83XT6								Q83XT2	Q83XT2	44	21	100.0	71	2	Q83XT2	Q83XSS	Q83XSS	45	21	100.0	71	
Q83XT2								Q83XSS	Q83XSS	46												

RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	STRAIN=cy, Chinese Spring;	STRAIN=cy, Chinese Spring;
RA	Young D.A., Allen R., Harvey A.J., Lonsdale D.M.;	Young D.A., Allen R., Harvey A.J., Lonsdale D.M.;
RT	"Characterization of a Gene encoding a single-subunit RNA Polymerase from maize which is alternatively spliced";	"Characterization of a Gene encoding a single-subunit RNA Polymerase from maize which is alternatively spliced";
RT	from maize (which is alternatively spliced);	from maize (which is alternatively spliced);
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AU005344; CHA06439.1; -	EMBL: AU005344; CHA06439.1; -
DR	GO: GO:0003899; F DNA-directed RNA polymerase activity; IEA.	GO: GO:0003899; F DNA-directed RNA polymerase I activity; IEA.
DR	GO: GO:0003900; F DNA-directed RNA polymerase II activity; IEA.	GO: GO:0003900; F DNA-directed RNA polymerase II activity; IEA.
DR	GO: GO:0003902; F DNA-directed RNA polymerase III activity; IEA.	GO: GO:0003902; F DNA-directed RNA polymerase III activity; IEA.
DR	GO: GO:0016740; Extratransferase activity; IEA.	GO: GO:0016740; Extratransferase activity; IEA.
KW	Nuc-Lotidyltransferase; Transferase.	Nuc-Lotidyltransferase; Transferase.
FT	NON_TER	NON_TER
FT	1	1
FT	11	11
FT	11 AA;	1329 MW;
FT		CD96344923240AB2 CRC64;
SQ	Query Match	Score 21;
SQ	Best Local Similarity	DB 10;
SQ	Matches	Pred. No. 1.7e+02;
SQ	Conservative	Indels 0;
SQ		Gaps 0;

Qy	1 DEVD 4	Score 21;
Db		Best Local Similarity
Db	2 DEVD 5	Matches 0;

RESULT 2		RESULT 3		RESULT 4		RESULT 5		
Q51913	PRELIMINARY;	PRT;	44 AA.	Q97Q87	PRELIMINARY;	PRT;	45 AA.	
ID Q51913;				ID 097Q87				
AC 01-NOV-1996 (TREMBLrel. 01; Created)				AC 097Q87;				
DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)				DT 01-OCT-2001 (TREMBLrel. 18; Created)				
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)				DT 01-OCT-2001 (TREMBLrel. 18; Last sequence update)				
DE HMG-CoA reductase (Fragment).				DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)				
OS Pseudomonas mevalonii				DE Hypothetical protein SP1339.				
Bacteria; Proteobacteria.				GN SP1339.				
OX NCBI TaxID=2044;				OS Streptococcus pneumoniae.				
RN SEQUENCE FROM N.A.				OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
RX MEDLINE=90078086; PubMed=26872316;				OC Streptococcus.				
RA Anderson D.H.; Rodwell V.W.;				OC NCBI TaxID=1313;				
RT "Nucleotide sequence and expression in <i>Escherichia coli</i> of the 3'-hydroxy-3-methylglutaryl coenzyme A lyase gene of <i>Pseudomonas mevalonii</i> ".				RN [1] _				
RT J. Bacteriol. 171:6458-6472 (1989).				RP SEQUENCE FROM N.A.				
RL EMBL; M3107; AA2594; 1..				RC STRAIN=ATCC BAA-334 / TIGR4;				
DR GO:0004120; F:hydroxymethylglutaryl-CoA reductase (NADPH) . . . ; IEA.				RC MEDLINE=21335709; PubMed=11463916;				
DR GO:0009058; P:biosynthesis IEA.				RA Tettelin H.; Nelson K.E.; Paulsen I.T.; Eisen J.A.; Read T.D.; Petterkin S.; Heidelberg J.; DeBoy R.T.; Dodson R.J.; Durkin A.S.; Gwinn M.; Kolonay J.F.; Nelson W.C.; Peterson J.D.; Umayam L.A.; White O.; Salzberg S.L.; Lewis M.R.; Radune D.; McDonald L.A.; Wolf A.M.; Utterback T.R.; Hansen C.L.; Holt I.E.; Loftus B.J.; Feldblum T.V.; Angiuoli S.; Dickinson T.; Hickey E.K.; Dougherty B.A.; Morrison D.A.; Hollingshead S.K.; Fraser C.M.; RT "Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> ."				
DR InterPro; IPR022020; HMG-CoA_red.				RT pneumoiae;"				
DR InterPro; IPR009239; HMG-CoA_sub_bind.				RT Science 293:498-505(2001);				
DR PFam; PF003368; HMG-CoA_red; 1..				DR EMBL; AE007432; AAC/5437.1; -.				
FT NON_TER				DR PIR; D95155; D95155.				
SEQUENCE 44 AA; 4925 MW; 9722EE2A58DBE9193 CRC64;				DR TIGR; SP1339; -.				
Query Match Score 21; DB 2; Length 44;				DR Hypothetical protein; Complete proteome; SEQUENCE 45 AA; 5089 MW; F0A7B635C2683F20 CRC64;				
Best Local Similarity 100.0%; Prd. No. 7e+02;				DR RT pneumoiae;"				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				DR Best Local Similarity 100.0%; Prd. No. 7.2e+01; Mismatches 0; Indels 0; Gaps 0;				
Qy 1 DEVD 4				DR Query Match Score 21; DB 16; Length 45;				
Db 14 DEVD 17				DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
RESULT 2		RESULT 3		RESULT 4		RESULT 5		
Q49798	PRELIMINARY;	PRT;	45 AA.	QBFVIL6	PRELIMINARY;	PRT;	45 AA.	
ID Q49798;				ID QBFVIL6				
AC 01-JUN-1998 (TREMBLrel. 06; Created)				AC QBFVIL6				
DT 01-JUN-1998 (TREMBLrel. 06; Last sequence update)				DT 01-MAR-2003 (TREMBLrel. 23; Created)				
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)				DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)				
DE R2R3-MYB transcription factor (Fragment).				DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)				
GN ATMYB75.				DE Hypothetical protein.				
OS Arabidopsis thaliana (Mouse-ear cress).				GN BRA081.				
OC Eukaryota; Viridiplantae; Streptophytina; Tracheophyta;				OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC Spermatophyta; Magnoliophyta; eudicots; rosids;				OC Brucellaceae; Brucella.				
OC Brassidales; Brassicaceae; Arabidopsis.				OC NCBI TaxID=29461;				
OX NCBI_TaxID=3702;				RN [1] _				
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.				RP SEQUENCE FROM N.A.				
DR EMBL; Z95798; CAB09230; 1..				RC STRAIN=1330 / Bicvar 1;				
DR PROSITE; PS50090; MYB 3..1.				RC MEDLINE=2224771; PubMed=12271122;				
FT NON_TER	1..			RA Paulsen I.T.; Seshaadri R.; Nelson K.E.; Eisen J.A.; Heidelberg J.F.; Daugherty S.C.; DeBoy R.T.; Durkin A.S.; Kolonay J.P.; Madupu R.; Nelson W.C.; Ayodeji B.; Kraft M.; Shetty J.; Malek J.; Van Aken S.E.; Riedmiller S.; Tetzelin H.; Gill S.R.; White O.; Salzberg S.L.; Hoover D.L.; Lindler L.E.; Halling S.M.; Boyle S.M.; Fraser C.M.; RA "The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts".				
SQ SEQUENCE 45 AA; 5308 MW; ASABE1509F3D376 CRC64;	45			RT Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).				
Query Match Score 21; DB 10; Length 45;				RL EMBL; AE014576; AAC/3996.1; -.				
Best Local Similarity 100.0%; Prd. No. 7.2e+02;				DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				DR Query Match Score 21; DB 16; Length 45;				
Qy 1 DEVD 4				DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

DR TIGR; BRA0821; -.
 KW Hypothetical protein; Complete proteome;
 SEQUENCE 45 AA; 5041 MW; 7F2B6874E77F886 CRC64;
 Query Match Score 21; DB 16; Length 45;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 |||||
 Db 3 DEVD 6

RESULT 6
 Q96P95 PRELIMINARY; PRT; 49 AA.
 AC Q96P95; PRELIMINARY;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Poly (ADP-ribose) Polymerase (Fragment).
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.; Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.; Kim J.H.; Rattus.
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.; Kim J.H.; Rattus.
 RT "Characterization of TPA-responsive genes in U937 cells using ordered differential display PCR.";
 RT Submitted to the EMBL/GenBank/DDBJ databases.
 RL AF401218; AA02174.1; -.
 DR GO:0010533; C:nucleus; IEA.
 DR InterPro: IPR001510; Znf PolyADPpol.
 DR Pfam: PF00655; ZF-PARP; 1.
 DR PROSITE: PS50064; PARP_ZN_FINGER_2; 1.
 PT NON_TER 1 49
 PT NON_TER 1 49
 SQ SEQUENCE 49 AA; 5300 MW; 68F91BA7DADDFA5 CRC64;

Query Match Score 21; DB 4; Length 49;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 |||||
 Db 34 DEVD 37

RESULT 7
 Q9XVP5 PRELIMINARY; PRT; 49 AA.
 AC Q9XVP5; PRELIMINARY;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-003 (TREMBLrel. 24, Last annotation update)
 DE F35C12.1 protein.
 GN Caenorhabditis elegans.
 OS Caeorhabditis elegans.
 OC Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.
 OC Rhabditida; Pelioderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN
 RP SEQUENCE FROM N.A.; Baynes C.;
 RA Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.; Baynes C.;
 RX PubMed=19069613; Pred. No. 7.8e+02;
 RA none;
 RT "Genome sequence of the nematode *C. elegans*: A platform for

investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; CAB03046.1;
 DR PIR; T21746;
 DR WormPep; F35C12.1;
 SQ SEQUENCE 49 AA; 5537 MW; 778CB60EEB3DFFEBE CRC64;
 Query Match Score 21; DB 5; Length 49;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 |||||
 Db 33 DEVD 36

RESULT 8
 Q63952 PRELIMINARY; PRT; 50 AA.
 AC Q63952; PRELIMINARY;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Endoplasmic (Fragment).
 GN GRP94.
 OS Rattus sp.
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10181;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=8314313;
 RX MEDLINE=914828; De Young M.W.; Yamazaki A.; Bennett S.A.; Chen J.H.; Shwed P.S.; Couture C.; Birnboim H.C.; Immunoselection of GRP94/endoplasmic from a KNRK cell specific lambda phage library using antibodies directed against a putative heparanase amino-terminal peptide.; Int. J. Cancer 56 226-234 (1994).
 RA DR EMBL; S69315; AAB29919.2; -.
 RT FT NON_TER 50 50
 SQ SEQUENCE 50 AA; 5478 MW; D8866A965A646117 CRC64;

Query Match Score 21; DB 11; Length 50;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEVD 4
 |||||
 Db 23 DEVD 26

RESULT 9
 Q9IAB6 PRELIMINARY; PRT; 53 AA.
 AC Q9IAB6; PRELIMINARY;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Smx5 (Fragment).
 GN SMX5.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.; Suelthahn H.; Murray B.W.; Klein J.;
 RA "Analysis of Ancient Mhc Class III Synteny by Mapping of Orthologous Genes in the Zebrafish.";
 RT Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF210645; AAP0450.1;
 DR ZFIN; ZDB-GENE-000616-10; smx5.

DR GO:0005634; C:nucleus; IEA.
 DR GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
 DR GO:0008248; F:pre-mRNA splicing factor activity; IEA.
 DR GO:0008271; P:mRNA splicing; IEA.
 DR InterPro; IPR006649; snRNP.
 DR InterPro; IPR01163; snRNP_Sm.
 DR PF01423; LSM; 1.
 DR Prodrom; PDO0287; snRNP; 1.
 DR NON_TER 1 1
 FT NON_TER 53 53
 SQ SEQUENCE 53 AA; 6078 MW; E70502074A527393 CRC64;
 Query Match 100.0%; Score 21; DB 13; Length 53;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 48 DEVD 51
 RESULT 10
 Q981MB_ PRELIMINARY; PRT; 53 AA.
 ID Q981MB_
 AC Q981MB;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein msr2334.
 GN MSR2334.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=MSR2334; PubMed=3031099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idezawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti".
 RL DNA Res. 7(3):331-338 (2000).
 DR EMBL; AP02999; BAR4948; 1; .
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 53 AA; 5289 MW; B7CCB7886C6D8279 CRC64;
 Query Match 100.0%; Score 21; DB 16; Length 53;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 10 DEVD 13
 RESULT 11
 Q382558_ PRELIMINARY; PRT; 54 AA.
 ID Q382558;
 AC Q382558;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Unidentified ORF15.
 OS Lactococcus phage bIL67.
 OC ssDNA viruses; no RNA stage; Caudovirales; Siphoviridae;
 OC c2-like viruses.
 OX NCBI_TaxID=336343;
 RN [1] SEQUENCE FROM N.A.
 RP

RX MEDLINE=45111629; PubMed=7812447;
 RA Schouler C., Ehrlich S.D., Choppin M.C.; "Sequence and organization of the lactococcal prolate-headed bIL67 phage genome,"; Microbiology 140:1061-3069 (1994).
 RL EMBL; L31769; AAA74352; 1; .
 SQ SEQUENCE 54 AA; 63738 MW; F2D42F31659BF751 CRC64;
 Query Match 100.0%; Score 21; DB 9; Length 54;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 10 DEVD 13
 RESULT 12
 Q38280_ PRELIMINARY; PRT; 54 AA.
 ID Q38280;
 AC Q38280;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE B17 protein.
 OS Lactococcus bacteriophage c2
 OC ssDNA viruses; no RNA stage; Caudovirales; Siphoviridae;
 CC c2-like viruses.
 OX NCBI_TaxID=31537;
 RN [1] SEQUENCE FROM N.A. PubMed=8221377;
 RP SEQUENCE FROM N.A. PubMed=94036433; PubMed=94036433;
 RX MEDLINE=94036433; PubMed=94036433;
 RA Ward B.J., Beresford T.P., Lubbers M.W., Jarvis A.W.; "Sequence analysis of the lysis gene region of the prolate lactococcal bacteriophage c2"; Can. J. Microbiol. 39:767-774 (1993).
 RN [2] SEQUENCE FROM N.A. PubMed=7816023;
 RP SEQUENCE FROM N.A. PubMed=95115663; PubMed=95115663;
 RX MEDLINE=95115663; PubMed=95115663;
 RA Lubbers M.W., Ward B.J., Beresford T.P., Jarvis A.W.; "Sequencing and analysis of the cos region of the lactococcal bacteriophage c2"; Mol. Gen. Genet. 245:160-166 (1994).
 RN [3] SEQUENCE FROM N.A. PubMed=96086019; PubMed=96086019;
 RP SEQUENCE FROM N.A. PubMed=96086019; PubMed=96086019;
 RX MEDLINE=96086019; PubMed=96086019;
 RA Lubbers M.W., Waterfield N.R., Beresford T.P., Le Page R.W., Jarvis A.W.; "Sequencing and analysis of the prolate-headed lactococcal bacteriophage c2 genome and identification of the structural genes."; Appl. Environ. Microbiol. 61:4348-4356 (1995).
 DR EMBL; L48605; AAA9263; 1; .
 SQ SEQUENCE 54 AA; 6453 MW; EA5811217531P751 CRC64;
 Query Match 100.0%; Score 21; DB 9; Length 54;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEVD 4
 Db 10 DEVD 13
 RESULT 13
 Q8ANR3_ PRELIMINARY; PRT; 54 AA.
 ID Q8ANR3;
 AC Q8ANR3;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE P0034A04; 6 Protein.
 GN P0034A04.6.

OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantes; Streptophyta; Embryophytina; Tracheophytina;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=33947;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV; Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.; DNA, chromosome 7, PAC
 RT clone: P0334A04.;
 RT "Oryza sativa nippobare (GA3) genomic segments and development of
 an RT-PCR detection assay.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AP033433; BRC642.1;
 SQ SEQUENCE 54 AA; 6002 MW; 1B25F6484151E8B CRC64;
 Query Match Score 100.0%; Score 21; DB 10; Length 54;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;

RESULTS 14
 Q977A0 PRELIMINARY; PRT; 54 AA.
 ID Q977A0
 AC 0977A0:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative alcohol dehydrogenase.
 GN STS015.
 CS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=11955;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / '_;
 RX MEDLINE=22456116; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hoboyama A., Fukui S.,
 RA Nagai Y., Nishizima K., Otsuka R., Nakazawa H., Kato Y.,
 RA Yoshihizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Niishimura M., Yamagishi A.,
 RA Oshima T., Rikuchi H.,
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000981; BAB4994.1;
 DR GO: GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
 DR GO: GO:000270; F:zinc ion binding; IEA.
 DR InterPro; IPR00085; Adh_zinc_Family.
 DR Pfam; PF00107; ADH_zinc_N_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 54 AA; 6138 MW; 132BC067738F740 CRC64;
 Query Match Score 100.0%; Score 21; DB 17; Length 54;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;

RESULTS 15
 Q99H60 PRELIMINARY; PRT; 56 AA.
 ID Q99H60
 AC 099H60:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE RNA-dependent RNA polymerase (fragment).
 OS Human Picobirnavirus.
 OC Picobirnaviruses; dsRNA viruses; Picobirnavirus.
 OX NCBI_TaxID=145856;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=202-FL-97; PubMed=11080479;
 RX MEDLINE=20334978; Pubmed=11080479;
 RA Rosen B. I., Fang Z. Y., Glass R. I., Monroe S.S.;
 RT "Cloning of human picobirnavirus genomic segments and development of
 an RT-PCR detection assay.";
 RL Virology 277:316-329 (2000).
 DR EMBL: AF246935; AAC35379.1;
 DR GO; GO:003968; F:RNA-directed RNA polymerase activity; IEA.
 KW RNA-directed RNA polymerase.
 FT NON-TER 1 1
 FT NON-TER 56 56
 SQ SEQUENCE 56 AA; 6708 MW; 781490BF8BB423A9 CRC64;
 Query Match Score 100.0%;
 Best Local Similarity 100.0%;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;
 Qy 1 DEV D 4
 Db 35 DEV D 38
 Qy 1 DEV D 4
 Db 31 DEV D 34
 Search completed: May 24, 2004, 14:41:01
 Job time : 37.5 secs